

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 03:56:09 ; Search time 198 Seconds
(without alignments)
1276.973 Million cell updates/sec

Title: US-09-593-793A-l13
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLHRKRAQLL.....AIYFATQVVFQDKSLAKYSA 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	100.0	553	2 AAW69385	AAW69385 Prostate
2	2861	100.0	553	2 AAW71869	AAW71869 Amino aci
3	2861	100.0	553	3 AAY82002	AAY82002 Human Imm
4	2861	100.0	553	3 AAB28527	AAB28527 Protein e
5	2861	100.0	553	3 ABG94411	ABG94411 Human pro
6	2861	100.0	553	4 AAM01117	AAM01117 Human pro
7	2861	100.0	553	4 AAU69763	AAU69763 Human pro
8	2861	100.0	553	4 AAB74800	AAB74800 Prostate
9	2861	100.0	553	4 AAG99002	AAG99002 Human pro
10	2861	100.0	553	4 AAG62150	AAG62150 Human P50
11	2861	100.0	553	4 ABU71653	ABU71653 Prostate
12	2861	100.0	553	4 AAU04961	AAU04961 Human pro
13	2861	100.0	553	5 AAU10324	AAU10324 Human PRO
14	2861	100.0	553	5 ABR95222	ABR95222 Human L1-
15	2861	100.0	553	5 AAU82843	AAU82843 Human bre
16	2861	100.0	553	5 AAG66190	AAG66190 Prostate
17	2861	100.0	553	5 ABG76665	ABG76665 Prostate
18	2861	100.0	553	5 ABR77575	ABR77575 Human mas
19	2861	100.0	553	6 ABR54334	ABR54334 Prostate
20	2861	100.0	553	7 ADR13563	ADR13563 Human pro
21	2861	100.0	553	7 ADG25979	ADG25979 Human pro
22	2861	100.0	553	7 ADK68076	ADK68076 Novel NOV
23	2861	100.0	553	7 ADN39584	ADN39584 Cancer/an

24	2861	100.0	553	7 ADN39230	ADN39230 Cancer/an
25	2861	100.0	553	8 ADH10469	ADH10469 Human P50
26	2861	100.0	553	8 ADG74153	ADG74153 Human pro
27	2861	100.0	553	8 ADR49065	ADR49065 Human NOV
28	2861	100.0	553	9 AEA00147	AEA00147 Human TAT
29	2861	100.0	553	9 AEA00667	AEA00667 Human TAT
30	2861	100.0	553	10 AEF66260	Aef66260 Human pro
31	2861	100.0	553	8 ADR65983	ADR65983 Human pro
32	2861	100.0	560	8 ADR66881	ADR66881 Human pro
33	2861	100.0	560	8 ADH10472	ADH10472 Codon-opt
34	2861	100.0	694	8 ADH10472	ADH10472 Prostate
35	2861	100.0	1079	4 AAB74830	AAB74830 Prostate
36	2861	100.0	1079	4 ABU71860	ABU71860 Prostate
37	2856	99.8	553	10 AEF66853	Aef66853 Human pro
38	2773.5	96.9	553	8 ADG74151	ADG74151 Monkey pr
39	2704	94.5	685	8 ADH10457	ADH10457 Human P50
40	2619	91.5	553	8 ADG74149	ADG74149 Rat prost
41	2610	91.2	644	8 ADH10471	ADH10471 P501S-CPC
42	2610	91.2	644	8 ADH10470	ADH10470 CPC- P501
43	2610	91.2	652	8 ADH10467	ADH10467 CPC-P501S
44	2610	91.2	652	8 ADH10453	ADH10453 CPC- P501
45	2610	91.2	671	8 ADH10459	ADH10459 CPC- P501

ALIGNMENTS

RESULT 1
ID AAW69385 standard; protein; 553 AA.
XX AAW69385;
XX AC
XX AAW69385;
DT 25-MAR-2003 (revised)
DT 08-DEC-1998 (first entry)
XX
DE Prostate tumour specific gene clone L1-12 protein.

XX Prostate tumour specific gene; human; prostate cancer; detection; therapy.
XX Homo sapiens.
XX PN WO9837418-A2.
XX PD 27-AUG-1998.
XX PF 25-FEB-1998; 98WO-US003690.
XX PR 25-FEB-1997; 97US-00806596.
XX PR 01-AUG-1997; 97US-00904809.
XX PR 09-FEB-1998; 98US-00020747.
XX (CORI-) CORIXA CORP.

Xu J, Dillion DC;
WPI: 1998-480805/41.
N-PSDB; AAV58586.
Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers.

Example 1; Page 87-89; 141pp; English.

This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.

CC (Updated on 25-MAR-2003 to correct PR field.)		PA (CORI-) CORIXA CORP.	
XX	Sequence 553 AA;	XX	Xu J, Dillon DC;
SQ		XX	WPI; 1998-609886/51.
		DR	N-PSDB; AAV61201.
		XX	Polypeptides comprising immunogenic portions of prostate proteins - used
		PT	in a vaccine for the treatment of prostate cancer.
		XX	Example 1; Page 82-84; 130pp; English.
		XX	The present sequence is an immunogenic portion of a prostate tumour
		CC	protein. The immunogen, or the DNA encoding it, can be used as a vaccine
		CC	for the treatment of prostate cancer. The immunogen was isolated from a
		CC	prostate tumour cDNA library obtained by subtracting a prostate tumour
		CC	cDNA expression library with a normal tissue cDNA library
		XX	Sequence 553 AA;
		SQ	
Query Match 100.0%; Score 2861; DB 2; Length 553;		Query Match 100.0%; Score 2861; DB 2; Length 553;	
Best Local Similarity 100.0%; Pred. No. 2.1e-268;		Best Local Similarity 100.0%; Pred. No. 2.1e-268;	
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MVQRLWVSRLLRHKAQQLLVNLTFTGLEVCAGITVVPPLLEVGVEBKFTMTVLGIG 60	QY	1 MVQRLWVSRLLRHKAQQLLVNLTFTGLEVCAGITVVPPLLEVGVEBKFTMTVLGIG 60
DB	1 MVQRLWVSRLLRHKAQQLLVNLTFTGLEVCAGITVVPPLLEVGVEBKFTMTVLGIG 60	DB	1 MVQRLWVSRLLRHKAQQLLVNLTFTGLEVCAGITVVPPLLEVGVEBKFTMTVLGIG 60
QY	61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLCPDPRPL 120	QY	61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLCPDPRPL 120
DB	61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLCPDPRPL 120	DB	61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLCPDPRPL 120
QY	121 ELALLILGVGLLDFCGQVCFPTLEALLSDLPDPHCRQAYSVYAFMISLGGCLGYLLPA 180	QY	121 ELALLILGVGLLDFCGQVCFPTLEALLSDLPDPHCRQAYSVYAFMISLGGCLGYLLPA 180
DB	121 ELALLILGVGLLDFCGQVCFPTLEALLSDLPDPHCRQAYSVYAFMISLGGCLGYLLPA 180	DB	121 ELALLILGVGLLDFCGQVCFPTLEALLSDLPDPHCRQAYSVYAFMISLGGCLGYLLPA 180
QY	181 IDWTSALAPYLGTQECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240	QY	181 IDWTSALAPYLGTQECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
DB	181 IDWTSALAPYLGTQECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240	DB	181 IDWTSALAPYLGTQECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
QY	241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFVAELCSWMALMTFTLFTDFVGEGL 300	QY	241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFVAELCSWMALMTFTLFTDFVGEGL 300
DB	241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFVAELCSWMALMTFTLFTDFVGEGL 300	DB	241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFVAELCSWMALMTFTLFTDFVGEGL 300
QY	301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVSFLVMDRLVQRFGRTRAVYLVA 360	QY	301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVSFLVMDRLVQRFGRTRAVYLVA 360
DB	301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVSFLVMDRLVQRFGRTRAVYLVA 360	DB	301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVSFLVMDRLVQRFGRTRAVYLVA 360
QY	361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420	QY	361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB	361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420	DB	361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY	421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRRVVGEPTEA 480	QY	421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRRVVGEPTEA 480
DB	421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRRVVGEPTEA 480	DB	421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRRVVGEPTEA 480
QY	481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAYFATQ 540	QY	481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAYFATQ 540
DB	481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAYFATQ 540	DB	481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAYFATQ 540
QY	541 VVFDKSDLAKYSA 553	QY	541 VVFDKSDLAKYSA 553
DB	541 VVFDKSDLAKYSA 553	DB	541 VVFDKSDLAKYSA 553
RESULT 3		RESULT 3	
AA182002		AA182002	
ID AAY82002 standard; protein; 553 AA.		ID AAY82002 standard; protein; 553 AA.	
XX		XX	
AC		AC	
XX		XX	
DT		DT	
13-JUN-2000 (first entry)		13-JUN-2000 (first entry)	
XX		XX	

DE Human immunogenic prostate tumour protein sequence SEQ ID NO:113.
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine.
XX OS Homo sapiens.
XX PN WO200004149-A2.
XX PD 27-JAN-2000.
XX PF 14-JUL-1999; 99WO-US015838.
XX PR 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 98US-00232149.
PR 15-JAN-1999; 98US-00232880.
PR 09-APR-1999; 99US-00288946.
XX (CORI-) CORIXA CORP.
XX PA
XX PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX DR
XX PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX PS
XX Claim 3; Page 138-139; 263pp; English.
XX CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idiotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
XX the present invention
XX SQ Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHRKAQLLLNLLTFGLVCLAAAGITYVPPILLLEVGVEEKFMTWVLGIG 60
DB 1 MVQRLWVSRLLRHRKAQLLLNLLTFGLVCLAAAGITYVPPILLLEVGVEEKFMTWVLGIG 60
QY 61 PVILGLVCPVLGSGSDHMRGRRPFTWALSGLLSLFLIPRAGWLAGLLCPDRPL 120
DB 61 PVILGLVCPVLGSGSDHMRGRRPFTWALSGLLSLFLIPRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVLGDLFCQGVCTPLEALLSDLPDRDPCROAYSVYAFMISLGGCLGYP 180
DB 121 ELALLILGVLGDLFCQGVCTPLEALLSDLPDRDPCROAYSVYAFMISLGGCLGYP 180
QY 181 IDWDTSAAPYLGTQBECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
DB 181 IDWDTSAAPYLGTQBECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
QY 241 CCPCPARLAFNLGALLPRLHOLCCMRPTLRLFVAELCSWMLMTFTLFYTDVFGEL 300
DB 241 CCPCPARLAFNLGALLPRLHOLCCMRPTLRLFVAELCSWMLMTFTLFYTDVFGEL 300
QY 301 YQGVPRABPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360

DB 301 YQGVPRABPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360
QY 361 AFPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 AFPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYFATQ 540
DB 481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYFATQ 540
QY 541 VVFDKSLAKYSA 553
DB 541 VVFDKSLAKYSA 553
RESULT 4
AAB28527
ID AAB28527 standard; protein; 553 AA.
XX AC AAB28527;
XX DT 07-FEB-2001 (first entry)
XX DE Protein encoded by human breast tumour cDNA clone P501S.
XX KW Human; breast tumour antigen; cytostatic; immunotherapy; breast cancer;
KW vaccine.
XX OS Homo sapiens.
XX PN WO200061756-A2.
XX PD 19-OCT-2000.
XX PF 10-APR-2000; 2000WO-US009688.
XX PR 09-APR-1999; 99US-00288950.
XX PD 02-JUL-1999; 99US-00346327.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Xu J, Dillon DC;
XX WPI; 2000-638568/61.
DB N-PSDB; AAC79473.
PT A novel isolated polypeptide comprising an immunogenic portion of a
PT breast cancer protein useful in the detection and treatment of breast
PT cancer.
XX PS Claim 2; Page 92-93; 95pp; English.
XX CC The present sequence is encoded by a cDNA sequence which was isolated
CC from a breast tumour cDNA library. It is provided in a specification
CC relating to compounds for immunotherapy and diagnosis of breast cancer.
CC Breast tumour antigens and the polynucleotides that encode them may be
CC used in the production of a pharmaceutical composition to be used in the
CC treatment of breast cancer. Proliferated T cells and incubated antigen
CC presenting cells are also required. The polypeptides and polynucleotides
CC may also be used to produce a vaccine
XX SQ Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHRKAQLLLNLLTFGLVCLAAAGITYVPPILLLEVGVEEKFMTWVLGIG 60

[illegible][illegible]

```
OS Homo sapiens.
XX WO2001151633-A2.
XX
XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001WO-US001574.
XX
XX 14-JAN-2000; 2000US-00483672.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
XX Claim 2; Page 267-268; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) can be used for
XX monitoring the progression of cancer in a patient. (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate
XX volume. AAH93357 to AAH93944 and AAM0115 to AAM01318 represent
XX polynucleotide and amino acid sequences used in the exemplification of
XX the present invention
XX
XX Sequence 553 AA;
XX
XX *Query Match 100.0%; Score 2861; DB 4; Length 553;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-268;
XX Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MVQRLWVSRLLRHRAQALLVNLITFGLVCLAGITYVPPLLLLEVGVEEKPMTWLIGIG 60
DB 1 MVQRLWVSRLLRHRAQALLVNLITFGLVCLAGITYVPPLLLLEVGVEEKPMTWLIGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGLISLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGLISLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVLDFCGQVCFTEALSLDLPDPHCRQAYSVAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVLDFCGQVCFTEALSLDLPDPHCRQAYSVAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAAPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGTEPAEGLSAPLSPH 240
DB 181 IDWDTSAAPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGTEPAEGLSAPLSPH 240
QY 241 CCPCRARLAFRLNGLALLPRHLQCCMRPRTLRLFAELCSNMALMTFTLFTYDFVGEGL 300
DB 241 CCPCRARLAFRLNGLALLPRHLQCCMRPRTLRLFAELCSNMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLOCAISLVFSLVMDRLVQRFGRTRAVLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLOCAISLVFSLVMDRLVQRFGRTRAVLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALOILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALOILPYTLASLYHREKQVFLPKYRGDTGG 420
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QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEA 480
QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIVOLQSQSVTAYMVSAAGLGLVLIYFATQ 540
DB 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIVOLQSQSVTAYMVSAAGLGLVLIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553
XX
XX RESULT 7
XX ID AAU69763 standard; protein; 553 AA.
XX
XX AC AAU69763;
XX
XX 30-JAN-2002 (first entry)
XX
XX Human prostate cDNA encoded protein #3.
XX
XX Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
XX
XX Homo sapiens.
XX
XX WO200173032-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-US009919.
XX
XX 27-MAR-2000; 2000US-00536857.
XX
XX 09-MAY-2000; 2000US-00568100.
XX
XX 12-MAY-2000; 2000US-00570737.
XX
XX 13-JUN-2000; 2000US-00593793.
XX
XX 27-JUN-2000; 2000US-00605783.
XX
XX 09-AUG-2000; 2000US-00636215.
XX
XX 29-AUG-2000; 2000US-00651236.
XX
XX 06-SEP-2000; 2000US-00657279.
XX
XX 02-OCT-2000; 2000US-00679426.
XX
XX 10-OCT-2000; 2000US-00685166.
XX
XX 09-NOV-2000; 2000US-00709729.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX
XX N-PSDB; AAS63557.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 2; Page 269-270; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polypeptide of the invention
XX
XX Sequence 553 AA;
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	DR	WPI: 2001-245062/25.
	DR	N-PSDB; AAH02530.
	XX	Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
	PT	Claim 3; Page 157-158; 276pp; English.
	PS	The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of the cancer. Progression of a cancer, especially prostate cancer. AAH02422 to AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention
	CC	Sequence 553 AA;
	SQ	Query Match 100.0%; Score 2861; DB 4; Length 553; Best Local Similarity 100.0%; Pred. No. 2.le-268; Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MVQRLLWSRLHRKRAQLLVNLTFTGLEVCCLAGITVPPLLELVEGVEEKFMTWLIG 60
Dd	1	MVQRLLWSRLHRKRAQLLVNLTFTGLEVCCLAGITVPPLLELVEGVEEKFMTWLIG 60
Qy	61	PVLGLVCVPLLGSADHWGRYGRRRPFIWALSGLLSFLIPRAGWLAGLLCPDPRPL 120
Dd	61	PVLGLVCVPLLGSADHWGRYGRRRPFIWALSGLLSFLIPRAGWLAGLLCPDPRPL 120
Qy	121	ELALLTLGVLGLDFCGQCFTPLEALLSDLPDPCHCRQAQSVVAFMISLGCGLYLLPA 180
Dd	121	ELALLTLGVLGLDFCGQCFTPLEALLSDLPDPCHCRQAQSVVAFMISLGCGLYLLPA 180
Qy	181	IDWDTSSALAPYLGTQECLFGLLTILFCTCVAAATLLVAEEAALGTEPAEGLSAPSLSPH 240
Dd	181	IDWDTSSALAPYLGTQECLFGLLTILFCTCVAAATLLVAEEAALGTEPAEGLSAPSLSPH 240
Qy	241	CCPCRARLAFRNLGALLPRLHLQCCRMPTLRRLFVAELCSWMALMTFTFYDFVGSEGL 300
Dd	241	CCPCRARLAFRNLGALLPRLHLQCCRMPTLRRLFVAELCSWMALMTFTFYDFVGSEGL 300
Qy	301	YQGVPRAEPTGEARRHYDEGVGMGSLGLFLOCAISLVFSLVMDRLVQRFTRAVYLASVA 360
Dd	301	YQGVPRAEPTGEARRHYDEGVGMGSLGLFLOCAISLVFSLVMDRLVQRFTRAVYLASVA 360
Qy	361	AFVVAAGATCLSHSAVVATAAALTGFTFSALQILPYTLASLYHREKQVFPLPKYRGDTGG 420
Dd	361	AFVVAAGATCLSHSAVVATAAALTGFTFSALQILPYTLASLYHREKQVFPLPKYRGDTGG 420
Qy	421	ASSEDSIMTSFLPGPKGPAPFNHGHVAGSGSLPPPPALCCASACDVSRVVVWGEPTEA 480
Dd	421	ASSEDSIMTSFLPGPKGPAPFNHGHVAGSGSLPPPPALCCASACDVSRVVVWGEPTEA 480
Qy	481	RVPVGRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQSVTAAYMVSAAAGLGLVALIYFATQ 540
Dd	481	RVPVGRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQSVTAAYMVSAAAGLGLVALIYFATQ 540
Qy	541	VWFDKSDLAKYSA 553
Dd	541	VWFDKSDLAKYSA 553
		RESULT 9 AAG99002 standard; protein; 553 AA. XX

AC AAG99002;
XX 25-SEP-2001 (first entry)
XX Human prostate-specific amino acid sequence L1-12/P501S.
DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA.
XX Homo sapiens.
OS
XX WO200134802-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US030904.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX Claim 3; Page 167-168; 325pp; English.
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLRHRKAQALLNLLTFGLVCLAAAGITYVPPLLLEVGVEEKEFTWVLGIG 60
Db 1 MVORLWVSRLLRHRKAQALLNLLTFGLVCLAAAGITYVPPLLLEVGVEEKEFTWVLGIG 60
QY 61 PVGLVCVPLLCASDHWGRYGRBRPFTWALSGLTLLSLFLI PRAGWLAGLLCPDPRPL 120
Db 61 PVGLVCVPLLCASDHWGRYGRBRPFTWALSGLTLLSLFLI PRAGWLAGLLCPDPRPL 120
QY 121 ELALITLGVGLDFGQVCFCTPLEALLSLDFDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALITLGVGLDFGQVCFCTPLEALLSLDFDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTOECLFGLLTILFICVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTOECLFGLLTILFICVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCARLAFRLGALLPRLHOLCCMPRTLRFLVAELCSNMALMTFTFLFYDFVGEGL 300
Db 241 CCPCARLAFRLGALLPRLHOLCCMPRTLRFLVAELCSNMALMTFTFLFYDFVGEGL 300

QY 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
QY 361 APPVAAAGATCLSHSVAVVTASAAITGFTFSALQIILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAAGATCLSHSVAVVTASAAITGFTFSALQIILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGSEPTA 480
Db 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGSEPTA 480
QY 481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIIVLSQSVTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIIVLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553
RESULT 10
AAG62150
XX ID AAG62150 standard; protein; 553 AA.
XX AC AAG62150;
XX 06-JUL-2001 (first entry)
XX Human P501S inventive antigen SEQ ID NO: 333.
DE Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor.
XX Homo sapiens.
OS
XX WO200125273-A2.
XX 12-APR-2001.
XX 04-OCT-2000; 2000WO-US027465.
XX 04-OCT-1999; 99US-0157459P.
XX (CORI-) CORIXA CORP.
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX WPI; 2001-328324/34.
XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WTI.
XX Disclosure; Page 212-213; 228pp; English.
XX The present invention describes compositions comprising peptides derived
CC from the wilm's tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a polypeptide described in the exemplification of the invention
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLRHRKAQALLNLLTFGLVCLAAAGITYVPPLLLEVGVEEKEFTWVLGIG 60

Db		1	MVQRLWVSRLLRHRKAQLLVNLTLTFGLVCLAAAGITYVPPLLLLEVGVEEKFTMTVLGIG	60
Qy		61	PVLGLVCVPLIGSASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCCDPRLP	120
Db		61	PVLGLVCVPLIGSASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCCDPRLP	120
Qy		121	ELALLILGVGLDFCGQVCFTEPLEALLSDLPDRPDHCRQAYSVYAFMISLGGCLGYLLPA	180
Db		121	ELALLILGVGLDFCGQVCFTEPLEALLSDLPDRPDHCRQAYSVYAFMISLGGCLGYLLPA	180
Qy		181	IDWDTSAAPYLGTOBECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGUSAPLSPH	240
Db		181	IDWDTSAAPYLGTOBECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGUSAPLSPH	240
Qy		241	CCPCRARLAFRNIGALLPRLHOLCCRMPTLRLRFLVAELCSNMALMTFTLFYDFVGEGL	300
Db		241	CCPCRARLAFRNIGALLPRLHOLCCRMPTLRLRFLVAELCSNMALMTFTLFYDFVGEGL	300
Qy		301	YQGVPRAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYASVA	360
Db		301	YQGVPRAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYASVA	360
Qy		361	APFVAAGATCLSHSVAVVTASALTCFTFSALQILPYTLIASLYHREKQVFLPKYRGDTGG	420
Db		361	APFVAAGATCLSHSVAVVTASALTCFTFSALQILPYTLIASLYHREKQVFLPKYRGDTGG	420
Qy		421	ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRRVVVGEPTA	480
Db		421	ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRRVVVGEPTA	480
Qy		481	RVPVGRGICLDLAILDSAFLLSQVAPSLPMGSIIVQLSQSVTAYMYSAAGLGLVAFATQ	540
Db		481	RVPVGRGICLDLAILDSAFLLSQVAPSLPMGSIIVQLSQSVTAYMYSAAGLGLVAFATQ	540
Qy		541	VVPDKSDLAKYSA	553
Db		541	VVPDKSDLAKYSA	553
RESULT 11				
Id	ABU71653	standard; protein; 553 AA.		
Xx				
Ac	ABU71653;			
Xc				
Dt	10-JUN-2003 (first entry)			
Xt				
De	Prostate cancer specific antigen P501s.			
Xw				
Kw	Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;			
Kw	immunogen; cancer; prostate specific antigen.			
Os	Homo sapiens.			
Os	Synthetic.			
Xx	US2002192763-A1.			
Pn				
Xp	19-DEC-2002.			
Xx				
Pf	29-JUN-2001; 2001US-00895793.			
Xx				
Pr	04-OCT-1999; 99US-0157455P.			
Pr	04-OCT-2000; 2000US-00679272.			
Pr	28-MAR-2001; 2001US-00822827.			
Xx	(XUJJ/) XU J.			
Pa	(DILL/) DILLON D C.			
Pa	(MITC/) MITCHAM J L.			
Pa	(HARL/) HARLOCKER S L.			
Pa	(JIAN/) JIANG Y.			
Pa	(KALO/) KALOS M D.			
Pa	(FANG/) FANGER G R.			
Pa	(RETT/) RETTER M W.			

PA	(STOL/) STOLK J A.	
PA	(DAYC/) DAY C H.	
PA	(VEDV/) VEDVICK T S.	
PA	(CART/) CARTER D.	
PA	(LISX/) LI S X.	
PA	(WANG/) WANG A.	
PA	(SKEI/) SKEIKY Y A W.	
PA	(HEPL/) HEPLER W T.	
PA	(HEND/) HENDERSON R A.	
PA	(HURA/) HURAL J.	
PA	(MCNE/) MCNEILL P D.	
PA	(HOUG/) HOUGHTON R L.	
PA	(DEAS/) Y DE BASSOLS C V.	
PA	(FOYT/) FOY T M.	
XX		
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;	
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;	
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;	
PI	Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;	
XX		
DR	WPI; 2001-245062/25.	
XX		
PT	Prostate specific protein and its encoding polynucleotide, useful for the	
PT	treatment and diagnosis of prostate cancer.	
XX		
PS	Example 1; Fig 9; 85pp; English.	
XX		
CC	The invention describes a fusion protein comprising at least one amino	
CC	acid sequence of immunogenic portions of any of the 3 sequences not	
CC	defined in the specification, or sequences having at least 70 or 90 %	
CC	sequence identity to any one of the 35 nucleotide sequences defined in the USPTO web	
CC	site, which is encoded by any of the 4 nucleotide sequences not defined	
CC	in the specification. The fusion protein, composition and methods are	
CC	useful for diagnosing, preventing and/or treating cancer, particularly	
CC	prostate cancer. The proteins are useful as markers to indicate the	
CC	presence or absence of cancer. This is the amino acid sequence of a	
CC	prostate cancer specific antigen. Note: The sequence data for this patent	
CC	did not form part of the printed specification, but was obtained in	
CC	electronic format directly from the US patent office at	
CC	seqdata.uspto.gov/sequence.html?DocID=U620020192763	
XX		
SQ	Sequence 553 AA;	
Query Match 100.0%; Score 2861; DB 4; Length 553;		
Best Local Similarity 100.0%; Pred. No. 2.1e-268;		
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MVQRLWVSRLLRHRKAQLLVNLTLTFGLVCLAAAGITYVPPLLLLEVGVEEKFTMTVLGIG 60
Db	1	MVQRLWVSRLLRHRKAQLLVNLTLTFGLVCLAAAGITYVPPLLLLEVGVEEKFTMTVLGIG 60
Qy	61	PVLGLVCVPLIGSASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCCDPRLP 120
Db	61	PVLGLVCVPLIGSASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCCDPRLP 120
Qy	121	ELALLILGVGLDFCGQVCFTEPLEALLSDLPDRPDHCRQAYSVYAFMISLGGCLGYLLPA 180
Db	121	ELALLILGVGLDFCGQVCFTEPLEALLSDLPDRPDHCRQAYSVYAFMISLGGCLGYLLPA 180
Qy	181	IDWDTSAAPYLGTOBECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGUSAPLSPH 240
Db	181	IDWDTSAAPYLGTOBECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGUSAPLSPH 240
Qy	241	CCPCRARLAFRNIGALLPRLHOLCCRMPTLRLRFLVAELCSNMALMTFTLFYDFVGEGL 300
Db	241	CCPCRARLAFRNIGALLPRLHOLCCRMPTLRLRFLVAELCSNMALMTFTLFYDFVGEGL 300
Qy	301	YQGVPRAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYASVA 360
Db	301	YQGVPRAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYASVA 360
Qy	361	APFVAAGATCLSHSVAVVTASALTCFTFSALQILPYTLIASLYHREKQVFLPKYRGDTGG 420


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Db 361 APPVAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSMTSFLPGPKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSMTSFLPGPKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 12
AAU04961
ID AAU04961 standard; protein; 553 AA.
AC AAU04961;
XX
XX 24-OCT-2001 (first entry)
XX
DE Human prostate tumour protein L1-12.
KW Human; prostate tumour protein; prostate cancer.
XX Homo sapiens.
XX
PN US626245-B1.
XX
XX 17-JUL-2001.
XX
XX 25-FEB-1998; 98US-00030607.
XX
XX 25-FEB-1997; 97US-00806099.
XX
XX 01-AUG-1997; 97US-00904804.
XX
XX 09-FEB-1998; 98US-00020956.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC;
XX
XX WPI; 2001-440862/47.
XX
XX N-PSDB; AAS10108.
XX
XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumor protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient.
XX
XX Example 1; Col 125-127; 105pp; English.
XX
XX The sequence is a partial prostate tumour protein, encoded by a prostate
CC tumour specific cDNA. The DNA is useful for inhibiting the development of
CC prostate cancer or for treating prostate cancer in a patient
XX
XX Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. NO. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHRKAQLLLVNLFTFGLBVCLAAAGTIVVPLLLEGVBEKEFTMWLIGIG 60
Db 1 MVQRLWVSRLLRHRKAQLLLVNLFTFGLBVCLAAAGTIVVPLLLEGVBEKEFTMWLIGIG 60
QY 61 PVLLGVCVPLLSASDHNRGRRRPFITWALSGLLSLFLIPRAGMWLAGLLCPDPRPL 120
Db 61 PVLLGVCVPLLSASDHNRGRRRPFITWALSGLLSLFLIPRAGMWLAGLLCPDPRPL 120
QY 121 ELALLILVGLLDPCGVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILVGLLDPCGVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
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QY 181 IDWDTSALAPYLGTQEECLFGLTLTIFLTVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWDTSALAPYLGTQEECLFGLTLTIFLTVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCRARLAFRNILGALLPRLHQLCCRMPTLRLRFLVABELCSMMALMTTTLFTYDFVGEGL 300
Db 241 CCPCRARLAFRNILGALLPRLHQLCCRMPTLRLRFLVABELCSMMALMTTTLFTYDFVGEGL 300
QY 301 YQGVPRAPGPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 360
Db 301 YQGVPRAPGPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 360
QY 361 APPVAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSMTSFLPGPKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSMTSFLPGPKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 13
AAU10324
ID AAU10324 standard; protein; 553 AA.
XX
XX AC AAU10324;
XX
XX 14-FEB-2002 (first entry)
XX
XX Human PROST 03.
XX
XX Human; PROST 03; metastasis; prostate cancer; tumour; immune response;
KW cytostatic; vaccine.
XX
XX Homo sapiens.
XX
XX WO200181577-A2.
XX
XX 01-NOV-2001.
XX
XX 26-APR-2001; 2001WO-US013323.
XX
XX 27-APR-2000; 2000US-0200065P.
XX
XX 20-APR-2001; 2001US-00838785.
XX
XX (SCHD ) SCHERING AG.
XX
XX Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Steinbrecher R;
PI Van Heuit PT, Wu J;
XX
XX WPI; 2002-041404/05.
XX
XX N-PSDB; AAS14962.
XX
XX Novel PROST 03 polypeptides and polynucleotides useful in research,
PT diagnosis and therapeutic applications, particularly for use in cancer
PT therapeutics.
XX
XX Claim 14; Fig 2; 77pp; English.
XX
XX The invention relates to an isolated PROST 03 polypeptide (I) and to the
CC polynucleotide (II) encoding PROST 03. Fragments of (I) were used to
CC generate antibodies (III) to PROST 03. (III) is useful for selectively
CC destroying a cell expressing (I), and for treating a disease-state
CC associated with expression of PROST 03 in a human patient. (III) is
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CC useful for diagnosing metastasis associated with (I), in a subject. (I)
CC is also useful for diagnosing and treating diseases of cell proliferation
CC such as prostate cancers. (I) is also useful for generating antibodies to
CC PROST 03. (III) is useful in detecting the levels of PROST 03
CC polypeptides in cells and tissues, and in targeting drugs to primary and
CC metastatic tumours. (I) is also useful for stimulating immune response to
CC PROST 03 containing cells. (II) is useful in diagnostic assays for
CC detecting the levels of polynucleotides encoding PROST 03 in cells and
CC tissues. (II) is useful as DNA probes, as targets for antisense and
CC ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents the
CC amino acid sequence of human PROST 03
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLVSRLLRHRKAQLLLVLLTFTGLEVCLAAAGITYVPPLLLEVGBEKFMTVMVLGIG 60
Db 1 MVQRLVSRLLRHRKAQLLLVLLTFTGLEVCLAAAGITYVPPLLLEVGBEKFMTVMVLGIG 60

QY 61 PVGLGVCVPLGSDHWRGRRPFTWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVGLGVCVPLGSDHWRGRRPFTWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120

QY 121 ELALLIGVGLLDFCQVCFTPEALLSDLFDPDHCRAQSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLIGVGLLDFCQVCFTPEALLSDLFDPDHCRAQSVYAFMISLGGCLGYLLPA 180

QY 181 IDWTSALAPYLGTQECFLGGLTLFLTCVAATLLVABEALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTQECFLGGLTLFLTCVAATLLVABEALGPTPEAGLSAPLSLSPH 240

QY 241 CCPCRLARLFRNLGALLPRHLQCCRMPTLRLFVAELCSWMLMTFTFLTFDFVGEGL 300
Db 241 CCPCRLARLFRNLGALLPRHLQCCRMPTLRLFVAELCSWMLMTFTFLTFDFVGEGL 300

QY 301 YQGVPAEPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASYA 360
Db 301 YQGVPAEPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASYA 360

QY 361 APFVAAGATCLSHVAVVTASAAALGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APFVAAGATCLSHVAVVTASAAALGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420

QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480

QY 481 RVVPGRGICLDIALDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAGLGLVAFYATQ 540
Db 481 RVVPGRGICLDIALDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAGLGLVAFYATQ 540

QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 14
ABB95222
ID ABB95222 standard; protein; 553 AA.
XX
AC ABB95222;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human L1-12 protein SEQ ID NO 113.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy.

Query Match 100.0%; Score 2861; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Homo sapiens.
OS US2002022248-A1.
PN
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
XX(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
Fanger GR, Retter MW, Scolk JA, Day CH, Vedvick TS, Carter D;
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
WPI; 2002-255649/30.

New prostate-specific polynucleotides for diagnosing and treating
diseases, in particular prostate cancer, and as markers for the
progression of cancer.

Claim 2; SEQ ID NO 113; 87pp; English.

The present invention provides prostate-specific coding sequences and
their encoded proteins. These can be used in the diagnosis and treatment
of cancers, particularly prostate cancer. The present sequence is a
protein described in the invention

SQ Sequence 553 AA;

QY 1 MVQRLWVSRLRHRKAQALLVNLTLFGLVCLAAAGITYVPPLLLLEGVVEKEFTMTVLGIG 60
Db |
1 MVQRLWVSRLRHRKAQALLVNLTLFGLVCLAAAGITYVPPLLLLEGVVEKEFTMTVLGIG 60
QY 61 PVGLVCPVPLLSASDHWRGRRRPFITWALSGLISLSLFIIPRAGMWLAGLLCPDPRPL 120
Db |
61 PVGLVCPVPLLSASDHWRGRRRPFITWALSGLISLSLFIIPRAGMWLAGLLCPDPRPL 120
QY 121 ELALLILGVGLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
Db |
121 ELALLILGVGLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAALPYLGTQECLFGLLTIFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
Db |
181 IDWDTSAALPYLGTQECLFGLLTIFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
QY 241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
Db |
241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 360
Db |
301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db |
361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSLGFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 480
Db |
421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSLGFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 480
QY 481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIIVOLSQSVTAYMYSAAAGLGLVAYFATQ 540
Db |
481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIIVOLSQSVTAYMYSAAAGLGLVAYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db |
541 VVFDKSDLAKYSA 553

RESULT 15
AAU82643
ID AAU82643 standard; peptide; 553 AA.
XX
AC AAU82643;
XX
DT 23-APR-2002 (first entry)
XX
DE Human breast tumour polypeptide clone #3.
XX
KW Human; breast tumour polypeptide; breast cancer; cytostatic;
KW immunostimulant.
XX
OS Homo sapiens.
XX
PN WO2001198339-A2.
XX
PD 27-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-US019032.
XX
PR 22-JUN-2000; 2000US-00602877.
PR 12-OCT-2000; 2000US-00687507.
PR 06-FEB-2001; 2001US-00778381.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX
DR WPI; 2002-147792/19.
DR N-PSDB; ABK29012.
XX

PT Polynucleotides encoding breast tumor polypeptides, useful for treating
PT breast cancer or stimulating an immune response.
XX Claim 2; Page 144-145; 150pp; English.
XX The invention relates to polynucleotides encoding breast tumour
CC polypeptides. The sequences are useful for treating cancer, preferably
CC breast cancer, in a patient or for stimulating an immune response. The
CC polynucleotides and polypeptides are also useful in the diagnosis and
CC monitoring of breast cancer. A method for detecting the presence of a
CC cancer in a patient, comprises obtaining a biological sample from the
CC patient, contacting the biological sample with a binding agent that binds
CC to a breast tumour polypeptide, detecting in the sample an amount of
CC polypeptide that binds to the binding agent, and comparing the amount of
CC polypeptide to a predetermined cut-off value, therefore determining the
CC presence of a cancer in the patient. Sequences AAU82641-AAU82655
XX represent human breast tumour polypeptides of the invention
SQ Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0;
QY 1 MVQRLWVSRLRHRKAQALLVNLTLFGLVCLAAAGITYVPPLLLLEGVVEKEFTMTVLGIG 60
Db |
1 MVQRLWVSRLRHRKAQALLVNLTLFGLVCLAAAGITYVPPLLLLEGVVEKEFTMTVLGIG 60
QY 61 PVGLVCPVPLLSASDHWRGRRRPFITWALSGLISLSLFIIPRAGMWLAGLLCPDPRPL 120
Db |
61 PVGLVCPVPLLSASDHWRGRRRPFITWALSGLISLSLFIIPRAGMWLAGLLCPDPRPL 120
QY 121 ELALLILGVGLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
Db |
121 ELALLILGVGLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAALPYLGTQECLFGLLTIFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
Db |
181 IDWDTSAALPYLGTQECLFGLLTIFLTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
QY 241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
Db |
241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 360
Db |
301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db |
361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSLGFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 480
Db |
421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSLGFLQCAISLVFSLVMDRLVORFGTRAVYLASVA 480
QY 481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIIVOLSQSVTAYMYSAAAGLGLVAYFATQ 540
Db |
481 RVVPGRGICLDLAILDSAPLSQVAPSLFMGSIIVOLSQSVTAYMYSAAAGLGLVAYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db |
541 VVFDKSDLAKYSA 553

Search completed: May 27, 2006, 03:59:38
Job time : 203 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 04:05:04 ; Search time 50 Seconds
(without alignments)
968,089 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLRHRKAQLLL.....AIYFATQVVDKSLAKYSA 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2861	100.0	553	2	US-09-020-956-113 Sequence 113, App
2	2861	100.0	553	2	US-09-030-607-113 Sequence 113, App
3	2861	100.0	553	2	US-09-439-313-113 Sequence 113, App
4	2861	100.0	553	2	US-09-352-616A-113 Sequence 113, App
5	2861	100.0	553	2	US-09-602-877A-101 Sequence 101, App
6	2861	100.0	553	2	US-09-232-149A-113 Sequence 113, App
7	2861	100.0	553	2	US-09-159-812-113 Sequence 113, App
8	2861	100.0	553	2	US-09-636-215-113 Sequence 113, App
9	2861	100.0	553	2	US-09-685-166A-113 Sequence 113, App
10	2861	100.0	553	2	US-09-115-453-113 Sequence 113, App
11	2861	100.0	553	2	US-09-688-489-113 Sequence 113, App
12	2861	100.0	553	2	US-09-679-426-113 Sequence 113, App
13	2861	100.0	553	2	US-09-759-143-113 Sequence 113, App
14	2861	100.0	553	2	US-09-651-236-113 Sequence 113, App
15	2861	100.0	553	2	US-09-030-606-113 Sequence 113, App
16	2861	100.0	553	2	US-09-657-279-113 Sequence 113, App
17	2861	100.0	553	2	US-10-012-896-113 Sequence 113, App
18	2861	100.0	553	3	US-09-116-134-113 Sequence 113, App
19	2861	100.0	553	3	US-10-144-678A-113 Sequence 113, App
20	1517	53.0	305	3	US-10-144-678A-1029 Sequence 1028, App
21	1417.5	49.5	371	2	US-09-636-215-708 Sequence 708, App
22	1417.5	49.5	371	2	US-09-685-166A-708 Sequence 708, App
23	1417.5	49.5	371	2	US-09-679-426-708 Sequence 708, App
24	1417.5	49.5	371	2	US-09-759-143-708 Sequence 708, App
25	1417.5	49.5	371	2	US-09-651-236-708 Sequence 708, App
26	1417.5	49.5	371	2	US-09-657-279-708 Sequence 708, App

Sequence 708, App
Sequence 708, App
Sequence 852, App
Sequence 852, App
Sequence 852, App
Sequence 852, App
Sequence 852, App
Sequence 852, App
Sequence 852, App
Sequence 852, App
Sequence 36, Appl
Sequence 1028, Ap
Sequence 1011, Ap
Sequence 1011, Ap
Sequence 571, App
Sequence 706, App
Sequence 706, App
Sequence 706, App

ALIGNMENTS

RESULT 1
US-09-020-956-113
; Sequence 113, Application US/09020956
; Patent No. 6261582
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLLRHRKAQLLLNLLFTGLFVLCVLAAGITYVPPLLLLLVGVVEKEKMTWVLGIG 60
|||||

1 MVQRLWVSRLRRHKAQALLVNLLTFGLEVCIAAGITYVPPLLLLEVGVEEKFMVMTVLGIG 60
Db
61 PVLGLVCVPLLGASDHWRGRRPFIWALSGLILLSFLI PRAGWLAGLLCPDRPL 120
QY
61 PVLGLVCVPLLGASDHWRGRRPFIWALSGLILLSFLI PRAGWLAGLLCPDRPL 120
Db
121 ELALLILGVGLDFCGQVCFTEALLSDLPDPDCHCRQAYSVYAFMISLGGCIGYLLPA 180
QY
121 ELALLILGVGLDFCGQVCFTEALLSDLPDPDCHCRQAYSVYAFMISLGGCIGYLLPA 180
Db
181 IDWTSALAPYLGTOEBCIFGLLTFLITCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
QY
181 IDWTSALAPYLGTOEBCIFGLLTFLITCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
Db
241 CCPCRARLAFRNLCGALLPRHLQCCRMPTLRLFVAELCSMMALMTFTLFTDFVGEGL 300
QY
241 CCPCRARLAFRNLCGALLPRHLQCCRMPTLRLFVAELCSMMALMTFTLFTDFVGEGL 300
Db
301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
QY
301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
Db
361 AFVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY
361 AFVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db
421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY
421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db
481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIFYATQ 540
QY
481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIFYATQ 540
Db
541 VVFDKSDLAKYSA 553
QY
541 VVFDKSDLAKYSA 553
Db

RESULT 2
US-09-030-607-113
; Sequence 113, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0

QY 1 MVQRLWVSRLRRHKAQALLVNLLTFGLEVCIAAGITYVPPLLLLEVGVEEKFMVMTVLGIG 60
Db 1 MVQRLWVSRLRRHKAQALLVNLLTFGLEVCIAAGITYVPPLLLLEVGVEEKFMVMTVLGIG 60
QY 61 PVLGLVCVPLLGASDHWRGRRPFIWALSGLILLSFLI PRAGWLAGLLCPDRPL 120
Db 61 PVLGLVCVPLLGASDHWRGRRPFIWALSGLILLSFLI PRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFTEALLSDLPDPDCHCRQAYSVYAFMISLGGCIGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTEALLSDLPDPDCHCRQAYSVYAFMISLGGCIGYLLPA 180
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Db 181 IDWTSALAPYLGTOEBCIFGLLTFLITCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
QY 241 CCPCRARLAFRNLCGALLPRHLQCCRMPTLRLFVAELCSMMALMTFTLFTDFVGEGL 300
Db 241 CCPCRARLAFRNLCGALLPRHLQCCRMPTLRLFVAELCSMMALMTFTLFTDFVGEGL 300
QY 301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
Db 301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
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Db 361 AFVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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Db 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 3
US-09-439-313-113
; Sequence 113, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Panger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-439-313-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLLRHKAQALLVNLTLFGLVCLAAAGITYVPPILLLEVGVEKEKFTWVLGIG 60
Db 1 MVQRLWVSRLLRHKAQALLVNLTLFGLVCLAAAGITYVPPILLLEVGVEKEKFTWVLGIG 60
QY 61 PVGLVCVPLLGASDHMRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVGLVCVPLLGASDHMRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILVGLLDFCGQVCFPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILVGLLDFCGQVCFPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
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Db 241 CCPCRLARLAFNLGALLPRHLQCCRMPTLRLFVAELCSNMALMTFTLFYTDVFVGEGL 300
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Db 301 YGVVPAEPTGTRARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRGTAVYLSVA 360
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Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 4
US-09-352-616A-113
; Sequence 113, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113

; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-352-616A-113
Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLLRHKAQALLVNLTLFGLVCLAAAGITYVPPILLLEVGVEKEKFTWVLGIG 60
Db 1 MVQRLWVSRLLRHKAQALLVNLTLFGLVCLAAAGITYVPPILLLEVGVEKEKFTWVLGIG 60
QY 61 PVGLVCVPLLGASDHMRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVGLVCVPLLGASDHMRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILVGLLDFCGQVCFPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILVGLLDFCGQVCFPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTOECLFGLTLFLTCVAATLLVAEEAALGPTPEAEGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTOECLFGLTLFLTCVAATLLVAEEAALGPTPEAEGLSAPLSLSPH 240
QY 241 CCPCRLARLAFNLGALLPRHLQCCRMPTLRLFVAELCSNMALMTFTLFYTDVFVGEGL 300
Db 241 CCPCRLARLAFNLGALLPRHLQCCRMPTLRLFVAELCSNMALMTFTLFYTDVFVGEGL 300
QY 301 YGVVPAEPTGTRARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRGTAVYLSVA 360
Db 301 YGVVPAEPTGTRARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRGTAVYLSVA 360
QY 361 APVVAAGATCLSHVAVVTASAAALTGFTPSAQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APVVAAGATCLSHVAVVTASAAALTGFTPSAQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 5
US-09-602-877A-101
; Sequence 101, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-101
Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;

Db 181 IDWDTSAAPYLGTOECLFGLLTILFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
QY 241 CCPCRARLAFRNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
Db 241 CCPCRARLAFRNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
QY 301 YQGVPAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
Db 301 YQGVPAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 8

US-09-636-215-113
; Sequence 113, Application US/09636215
; Patent No. 6620922

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-636-215-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLHRKQAQLLVNLLTFGLVCLAAAGITYVPVLLLEGVBEKEKFWVLGIG 60
Db 1 MVQRLWVSRLLHRKQAQLLVNLLTFGLVCLAAAGITYVPVLLLEGVBEKEKFWVLGIG 60
QY 61 PVGLGVCVPLLSGSDHWRGRRPFTIWSLGLTILSLFLIPRAGWLAGLLCPDPRPL 120

Db 61 PVGLGVCVPLLSGSDHWRGRRPFTIWSLGLTILSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVLGDLFCGOVCFTPLEALLSDLFDPDPCRQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVLGDLFCGOVCFTPLEALLSDLFDPDPCRQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAAPYLGTOECLFGLLTILFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
Db 181 IDWDTSAAPYLGTOECLFGLLTILFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
QY 241 CCPCRARLAFRNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
Db 241 CCPCRARLAFRNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
QY 301 YQGVPAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
Db 301 YQGVPAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 9

US-09-685-166A-113
; Sequence 113, Application US/09685166A
; Patent No. 6630305

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-685-166A-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY		1	MVORLWVSRLLRHRAQAQLLIIVNLITFTGLEVCCLAAGITYVPPLLELVGVBEKFMTWLGIG	60
DB		1	MVORLWVSRLLRHRAQAQLLIIVNLITFTGLEVCCLAAGITYVPPLLELVGVBEKFMTWLGIG	60
QY		61	PVLGLVCVPLLGSASDHWGRGYRRRPFIIWALSIGILLSLFLIPRAGWLAGLLCPDRPPL	120
DB		61	PVLGLVCVPLLGSASDHWGRGYRRRPFIIWALSIGILLSLFLIPRAGWLAGLLCPDRPPL	120
QY		121	ELALLILVGULLDFCGQVCTPBLEALLSDIFRPDPCHCRQAYSIVAFMISLGCLGVLPLA	180
DB		121	ELALLILVGULLDFCGQVCTPBLEALLSDIFRPDPCHCRQAYSIVAFMISLGCLGVLPLA	180
QY		181	IDWDTSALAPYLGTQEELFGLLTLIFLTCVAATLLVAEBEAAALGPTEPAEGLSAPSLSPH	240
DB		181	IDWDTSALAPYLGTQEELFGLLTLIFLTCVAATLLVAEBEAAALGPTEPAEGLSAPSLSPH	240
QY		241	CCPCRARLAFRNLGALLPRLHLQCCRMPTLRLRLFVAELCSWMALMTFTLFYTFDFVEGL	300
DB		241	CCPCRARLAFRNLGALLPRLHLQCCRMPTLRLRLFVAELCSWMALMTFTLFYTFDFVEGL	300
QY		301	YQGVPPABEGTTRARHYDEGVNMSLGI.FLOCAISLVFSLVMORLVORFCTRAVIYLASVA	360
DB		301	YQGVPPABEGTTRARHYDEGVNMSLGI.FLOCAISLVFSLVMORLVORFCTRAVIYLASVA	360
QY		361	APFVAAGATC.LSHSVAVVTASAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG	420
DB		361	APFVAAGATC.LSHSVAVVTASAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG	420
QY		421	ASGEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPAPALCGASACDVSVRVVVGEPTEA	480
DB		421	ASGEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPAPALCGASACDVSVRVVVGEPTEA	480
QY		481	RVPVGRGICLDIAILD.SAFLLSOVAPSLFMGSI.VQLSQSVTAYMVSAAGLGLVAIFYAQ	540
DB		481	RVPVGRGICLDIAILD.SAFLLSOVAPSLFMGSI.VQLSQSVTAYMVSAAGLGLVAIFYAQ	540
QY		541	VFPDKSDLAKYSA 553 	
DB		541	VFPDKSDLAKYSA 553 	
 RESULT 10				
US-09-115-453-113				
; Sequence 113, Application US/09115453B				
; Patent No. 6657056				
; GENERAL INFORMATION:				
; APPLICANT: Xu, Jiangchun C.				
; APPLICANT: Dillon, Davin C.				
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND				
; TITLE OF INVENTION: METHODS FOR THEIR USE				
; FILE REFERENCE: 210121.427C4				
; CURRENT APPLICATION NUMBER: US/09/115,453B				
; CURRENT FILING DATE: 1998-07-14				
; NUMBER OF SEQ ID NOS: 228				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 113				
; LENGTH: 553				
; TYPE: PRT				
; ORGANISM: Homo sapien				
US-09-115-453-113				
 Query Match 100.0%; Score 2861; DB 2; Length 553;				
Best Local Similarity 100.0%; Pred. No. 1.5e-270;				
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
QY		1	MVORLWVSRLLRHRAQAQLLIIVNLITFTGLEVCCLAAGITYVPPLLELVGVBEKFMTWLGIG	60
DB		1	MVORLWVSRLLRHRAQAQLLIIVNLITFTGLEVCCLAAGITYVPPLLELVGVBEKFMTWLGIG	60
QY		61	PVLGLVCVPLLGSASDHWGRGYRRRPFIIWALSIGILLSLFLIPRAGWLAGLLCPDRPPL	120
DB		61	PVLGLVCVPLLGSASDHWGRGYRRRPFIIWALSIGILLSLFLIPRAGWLAGLLCPDRPPL	120
QY		121	ELALLILVGULLDFCGQVCTPBLEALLSDIFRPDPCHCRQAYSIVAFMISLGCLGVLPLA	180
DB		121	ELALLILVGULLDFCGQVCTPBLEALLSDIFRPDPCHCRQAYSIVAFMISLGCLGVLPLA	180
QY		181	IDWDTSALAPYLGTQEELFGLLTLIFLTCVAATLLVAEBEAAALGPTEPAEGLSAPSLSPH	240
DB		181	IDWDTSALAPYLGTQEELFGLLTLIFLTCVAATLLVAEBEAAALGPTEPAEGLSAPSLSPH	240
QY		241	CCPCRARLAFRNLGALLPRLHLQCCRMPTLRLRLFVAELCSWMALMTFTLFYTFDFVEGL	300
DB		241	CCPCRARLAFRNLGALLPRLHLQCCRMPTLRLRLFVAELCSWMALMTFTLFYTFDFVEGL	300
QY		301	YQGVPPABEGTTRARHYDEGVNMSLGI.FLOCAISLVFSLVMORLVORFCTRAVIYLASVA	360
DB		301	YQGVPPABEGTTRARHYDEGVNMSLGI.FLOCAISLVFSLVMORLVORFCTRAVIYLASVA	360
QY		361	APFVAAGATC.LSHSVAVVTASAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG	420
DB		361	APFVAAGATC.LSHSVAVVTASAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG	420
QY		421	ASGEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPAPALCGASACDVSVRVVVGEPTEA	480
DB		421	ASGEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPAPALCGASACDVSVRVVVGEPTEA	480
QY		481	RVPVGRGICLDIAILD.SAFLLSOVAPSLFMGSI.VQLSQSVTAYMVSAAGLGLVAIFYAQ	540
DB		481	RVPVGRGICLDIAILD.SAFLLSOVAPSLFMGSI.VQLSQSVTAYMVSAAGLGLVAIFYAQ	540
QY		541	VFPDKSDLAKYSA 553 	
DB		541	VFPDKSDLAKYSA 553 	
 RESULT 10				
US-09-115-453-113				
; Sequence 113, Application US/09115453B				
; Patent No. 6657056				
; GENERAL INFORMATION:				
; APPLICANT: Xu, Jiangchun C.				
; APPLICANT: Dillon, Davin C.				
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND				
; TITLE OF INVENTION: METHODS FOR THEIR USE				
; FILE REFERENCE: 210121.427C4				
; CURRENT APPLICATION NUMBER: US/09/115,453B				
; CURRENT FILING DATE: 1998-07-14				
; NUMBER OF SEQ ID NOS: 228				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 113				
; LENGTH: 553				
; TYPE: PRT				
; ORGANISM: Homo sapien				
US-09-115-453-113				
 Query Match 100.0%; Score 2861; DB 2; Length 553;				
Best Local Similarity 100.0%; Pred. No. 1.5e-270;				
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
QY		1	MVORLWVSRLLRHRAQAQLLIIVNLITFTGLEVCCLAAGITYVPPLLELVGVBEKFMTWLGIG	60
DB		1	MVORLWVSRLLRHRAQAQLLIIVNLITFTGLEVCCLAAGITYVPPLLELVGVBEKFMTWLGIG	60
QY		61	PVLGLVCVPLLGSASDHWGRGYRRRPFIIWALSIGILLSLFLIPRAGWLAGLLCPDRPPL	120
DB		61	PVLGLVCVPLLGSASDHWGRGYRRRPFIIWALSIGILLSLFLIPRAGWLAGLLCPDRPPL	120
QY		121		

Db 181 IDWTSALAPYLGTQBECLFGLLTLLIFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH 240
QY 241 CCPCRARLARFNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
Db 241 CCPCRARLARFNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
Db 301 YQGVPAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAIDLDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 12
US-09-679-426-113
; Sequence 113, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, John A.
; APPLICANT: Stolk, John H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-679-426-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLVWSRLRRHKAQLLVNLLTFGLVCLAAAGITYVPPLLLEVGVEEKEKMTWVLGIG 60
Db 1 MVQRLVWSRLRRHKAQLLVNLLTFGLVCLAAAGITYVPPLLLEVGVEEKEKMTWVLGIG 60
QY 61 PVGLGVCVPLLSGASDHWRGRRRPFITWALSGLTLLSLFLIPRAGWLAGLLCPDPREL 120
Db 61 PVGLGVCVPLLSGASDHWRGRRRPFITWALSGLTLLSLFLIPRAGWLAGLLCPDPREL 120

QY 121 ELALLILGVGLDFCGQVCFTPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTLLIFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH 240
Db 181 IDWTSALAPYLGTQBECLFGLLTLLIFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH 240
QY 241 CCPCRARLARFNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
Db 241 CCPCRARLARFNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
Db 301 YQGVPAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAIDLDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 13
US-09-759-143-113
; Sequence 113, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MVORLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITVVPPLLLLEVGVEEKFMTMWLGIG 60
1 MVORLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITVVPPLLLLEVGVEEKFMTMWLGIG 60
61 PVLGLVCVPLLSASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDRPL 120
61 PVLGLVCVPLLSASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDRPL 120
121 ELALLILGVGLDFCGQVCFPLEALLSDLPDRPDHCRQAYSVAFMISLGGCLGYLLPA 180
121 ELALLILGVGLDFCGQVCFPLEALLSDLPDRPDHCRQAYSVAFMISLGGCLGYLLPA 180
181 IDWDTSAAPYLGTQBECLFGLLTILFVLCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
181 IDWDTSAAPYLGTQBECLFGLLTILFVLCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
241 CCPCRLARLAFNLGALLPRLHQLCCMRPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
241 CCPCRLARLAFNLGALLPRLHQLCCMRPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
301 YQGVPRAEPTGTEARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRFSTRAVYLVA 360
301 YQGVPRAEPTGTEARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRFSTRAVYLVA 360
361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMWSAAGLGLVLIYFATQ 540
481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMWSAAGLGLVLIYFATQ 540
541 VVFDKSDLAKYSA 553
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RESULT 14
US-09-651-236-113
; Sequence 113, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651.236
; NUMBER OF SEQ ID NOS: 855
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT

; ORGANISM: Homo sapien
US-09-651-236-113
Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITVVPPLLLLEVGVEEKFMTMWLGIG 60
Db 1 MVORLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITVVPPLLLLEVGVEEKFMTMWLGIG 60
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Db 61 PVLGLVCVPLLSASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDRPL 120
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QY 181 IDWDTSAAPYLGTQBECLFGLLTILFVLCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
Db 181 IDWDTSAAPYLGTQBECLFGLLTILFVLCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
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Db 241 CCPCRLARLAFNLGALLPRLHQLCCMRPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
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Db 301 YQGVPRAEPTGTEARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRFSTRAVYLVA 360
QY 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMWSAAGLGLVLIYFATQ 540
Db 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMWSAAGLGLVLIYFATQ 540
541 VVFDKSDLAKYSA 553
541 VVFDKSDLAKYSA 553
RESULT 15
US-09-030-606-113
; Sequence 113, Application US/09030606
; Patent No. 6887660
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-606-113

Query Match		100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity		100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	MQVRLWVSLRLRHRKAQLLVNLLTFGLVCLAAAGITYVPPLLLEVGVEEKEFTMWVLGIG 60
Qy	61	PVLGLVCPVLLGSASDHWRGRRRPFVWALSGLLSLFLIPRAGWLAGLLCPDPRL 120
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Qy	121	ELALLILGVGLDFCQVCFTPLEALLSDLFRDPDHCROQSVYAFMISLGGCLGYLLPA 180
Db	121	ELALLILGVGLDFCQVCFTPLEALLSDLFRDPDHCROQSVYAFMISLGGCLGYLLPA 180
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Lb	181	IDWTSALAPYLGTOBECLFGLLTFLFTCVAAATLLVAEEAALGTEPAEGLSAPLSPH 240
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Db	241	CCPCRARLAFRNIGALLPRHLQCCRMPTLRLFVAELCSWMLMTFTLFTYDFVGEGL 300
Qy	301	YQGVPRAEPTGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLSVA 360
Db	301	YQGVPRAEPTGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLSVA 360
Qy	361	AFPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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Qy	421	ASSEDLSMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
Db	421	ASSEDLSMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
Qy	481	RVVPGRGICLDLAILDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db	481	RVVPGRGICLDLAILDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Qy	541	VVFDKSDLAKYSA 553
Db	541	VVFDKSDLAKYSA 553

Search completed: May 27, 2006, 04:06:28
Job time : 52 secs

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OM protein - protein search, using sw model

Run on: May 27, 2006, 04:05:48 ; Search time 183 Seconds
(without alignments)
1399.769 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLRHKAQLLL.....AIYFATQVVFDKSLAKYSA 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	100.0	553	US-09-745-288-101	Sequence 101, App
2	2861	100.0	553	US-09-838-785-2	Sequence 2, Appli
3	2861	100.0	553	US-09-759-143-113	Sequence 113, App
4	2861	100.0	553	US-09-780-669-113	Sequence 113, App
5	2861	100.0	553	US-09-030-606-113	Sequence 113, App
6	2861	100.0	553	US-09-822-827-113	Sequence 113, App
7	2861	100.0	553	US-09-115-453-113	Sequence 113, App
8	2861	100.0	553	US-09-232-880-113	Sequence 113, App
9	2861	100.0	553	US-09-895-793-113	Sequence 113, App
10	2861	100.0	553	US-09-895-814-113	Sequence 113, App
11	2861	100.0	553	US-10-012-896-113	Sequence 113, App
12	2861	100.0	553	US-10-010-940-113	Sequence 113, App
13	2861	100.0	553	US-10-144-678A-113	Sequence 113, App
14	2861	100.0	553	US-10-005-907-13	Sequence 13, Appl
15	2861	100.0	553	US-10-294-025-113	Sequence 113, App
16	2861	100.0	553	US-10-295-027-548	Sequence 548, App
17	2861	100.0	553	US-10-295-027-902	Sequence 902, App
18	2861	100.0	553	US-10-453-919-101	Sequence 101, App
19	2861	100.0	553	US-10-688-838-113	Sequence 113, App
20	2861	100.0	553	US-10-403-142-2	Sequence 2, Appli
21	2861	100.0	553	US-10-936-626-99	Sequence 99, Appl
22	2861	100.0	553	US-10-938-061-99	Sequence 99, Appl
23	2861	100.0	553	US-10-732-923-24012	Sequence 24012, A
24	2861	100.0	553	US-11-234-786-113	Sequence 113, App
25	2861	100.0	1079	US-09-822-827-947	Sequence 947, App
26	2861	100.0	1079	US-09-895-793-947	Sequence 947, App
27	2798	97.8	553	US-10-732-923-24008	Sequence 24008, A

ALIGNMENTS

RESULT 1

US-09-745-288-101
; Sequence 101, Application US/09745288
; Patent No. US20010018058A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-745-288-101

Query Match	100.0%	Score 2861	DB 3	Length 553
Best Local Similarity	100.0%	Pred No. 9,4e-240		
Matches 553	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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QY	61	61	61	61
QY	61	61	61	61
QY	121	121	121	121
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QY	181	181	181	181
QY	181	181	181	181
QY	241	241	241	241
QY	241	241	241	241
QY	301	301	301	301
QY	301	301	301	301
QY	361	361	361	361

Tue May 30 15:28:26 2006

Db 361 AFVPAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Qy 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRVVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRVVVVGEPTEA 480
Qy 481 RVVPGRGICLDLAILDSAFLLSQVAPSLPMGSIIVQLSQSVTAIYMSAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLPMGSIIVQLSQSVTAIYMSAAGLGLVAIFYATQ 540
Qy 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 3
US-09-759-143-113
; Sequence 113, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759.143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVORLWVSRLLRHRKAQLLVNLTLTFLGVLVCLAAAGITYVPPLLLEVGVEEKFMTMVLGIG 60
Db 1 MVORLWVSRLLRHRKAQLLVNLTLTFLGVLVCLAAAGITYVPPLLLEVGVEEKFMTMVLGIG 60
Qy 61 PVGLVVCVPLLGASDHWGRYGRRRPFIWALSIGLILSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVGLVVCVPLLGASDHWGRYGRRRPFIWALSIGLILSLFLIPRAGWLAGLLCPDPRPL 120
Qy 121 ELALLILGVLLDFCGQVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCIGLYLLPA 180
Db 121 ELALLILGVLLDFCGQVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCIGLYLLPA 180
Qy 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
Db 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
Qy 241 CCPCARLAFRNLGALLPRHLQCCMRPTRLRLFLVAELCSNMALMTFTLYTDFVGEGL 300
Db 241 CCPCARLAFRNLGALLPRHLQCCMRPTRLRLFLVAELCSNMALMTFTLYTDFVGEGL 300

Db 361 AFVPAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Qy 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRVVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSRVVVVGEPTEA 480
Qy 481 RVVPGRGICLDLAILDSAFLLSQVAPSLPMGSIIVQLSQSVTAIYMSAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLPMGSIIVQLSQSVTAIYMSAAGLGLVAIFYATQ 540
Qy 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

US-09-838-785-2
; Sequence 2, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
; APPLICANT: Lau, Ted
; APPLICANT: Lin, Rick
; APPLICANT: Parkes, Debbie
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinhrecher, Renate
; APPLICANT: Van Heuit, Pam T
; APPLICANT: Wu, John
; TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
; FILE REFERENCE: 51831AUSM1
; CURRENT APPLICATION NUMBER: US/09/838.785
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/200,065
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-838-785-2

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVORLWVSRLLRHRKAQLLVNLTLTFLGVLVCLAAAGITYVPPLLLEVGVEEKFMTMVLGIG 60
Db 1 MVORLWVSRLLRHRKAQLLVNLTLTFLGVLVCLAAAGITYVPPLLLEVGVEEKFMTMVLGIG 60
Qy 61 PVGLVVCVPLLGASDHWGRYGRRRPFIWALSIGLILSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVGLVVCVPLLGASDHWGRYGRRRPFIWALSIGLILSLFLIPRAGWLAGLLCPDPRPL 120
Qy 121 ELALLILGVLLDFCGQVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCIGLYLLPA 180
Db 121 ELALLILGVLLDFCGQVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCIGLYLLPA 180
Qy 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
Db 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
Qy 241 CCPCARLAFRNLGALLPRHLQCCMRPTRLRLFLVAELCSNMALMTFTLYTDFVGEGL 300
Db 241 CCPCARLAFRNLGALLPRHLQCCMRPTRLRLFLVAELCSNMALMTFTLYTDFVGEGL 300
Qy 301 YQGVPAEFGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLSVA 360
Db 301 YQGVPAEFGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLSVA 360
Qy 361 AFVPAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420

US-09-030-606-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLVWSRLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLLEVGVEEKFTMWLGIG 60
DB 1 MVQRLVWSRLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLLEVGVEEKFTMWLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVGLLDFCGQVCTPLEALLSDLFRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLLDFCGQVCTPLEALLSDLFRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
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QY 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLYTDFVGEGL 300
DB 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLYTDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
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DB 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553
RESULT 6
US-09-822-827-113
; Sequence 113, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 392
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-113
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLVWSRLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLLEVGVEEKFTMWLGIG 60
DB 1 MVQRLVWSRLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLLEVGVEEKFTMWLGIG 60

QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVGLLDFCGQVCTPLEALLSDLFRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
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QY 181 IDWDTSAALPYLGTQBECLFGLTLIFLTCVAATLLVAEEAALGPTPEAEGLSAPLSLSPH 240
DB 181 IDWDTSAALPYLGTQBECLFGLTLIFLTCVAATLLVAEEAALGPTPEAEGLSAPLSLSPH 240
QY 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLYTDFVGEGL 300
DB 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLYTDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIFYATQ 540
DB 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 7
US-09-115-453-113
; Sequence 113, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-115-453-113
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLVWSRLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLLEVGVEEKFTMWLGIG 60
DB 1 MVQRLVWSRLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLLEVGVEEKFTMWLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVGLLDFCGQVCTPLEALLSDLFRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLLDFCGQVCTPLEALLSDLFRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180

181	Qy	IDWDT	SALAPYLGTQEECLFGLLTILFTCVAATLLVAEEAALGPTPEAGLSAPSLSPH	240
181	Db	IDWDT	SALAPYLGTQEECLFGLLTILFTCVAATLLVAEEAALGPTPEAGLSAPSLSPH	240
241	Qy	CCPCR	ARLAFRNIGALLPRLHQLCRMPRTLRRLFVABELCSMWALMTFTFLFTDVFVGEGL	300
241	Db	CCPCR	ARLAFRNIGALLPRLHQLCRMPRTLRRLFVABELCSMWALMTFTFLFTDVFVGEGL	300
301	Qy	YQGV	PRAEPGTEARRHYDEGYRMSGSLGFLQCAISLVFSLVMDRLVQRFGTFAVYLASVA	360
301	Db	YQGV	PRAEPGTEARRHYDEGYRMSGSLGFLQCAISLVFSLVMDRLVQRFGTFAVYLASVA	360
361	Qy	APVAA	GATCTLSHSAVVVTTASAALTGFTFSALQIILPYTLASLYHREKOVFLPKYRGDTGG	420
361	Db	APVAA	GATCTLSHSAVVVTTASAALTGFTFSALQIILPYTLASLYHREKOVFLPKYRGDTGG	420
421	Qy	ASSED	SLMTSLPLPGPKAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA	480
421	Db	ASSED	SLMTSLPLPGPKAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA	480
481	Qy	RVPGR	GICDLAILDASFAFLSQVAPSLFMSGIVQLSQSVTAYMWSAAGLGLVATYFATQ	540
481	Db	RVPGR	GICDLAILDASFAFLSQVAPSLFMSGIVQLSQSVTAYMWSAAGLGLVATYFATQ	540
541	Qy	VVFDK	SOLAKYSA	553
541	Db	VVFDK	SOLAKYSA	553

RESULT 8

```

RES001 8
US-09-232-880-113
; Sequence 113, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-880-113

```

Query Match	100.0%	Score 2861;	DB 3;	Length 553;
Best Local Similarity	100.0%;	Pred. No. 9.4e-240;		
Matches 553; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MVQRLWSRLRHKRAQLLLVNLALTFGLEVCLAAAGITVVPPLLLEVGVEEKFMTMWLGIG	60	
Db	1	MVQRLWSRLRHKRAQLLLVNLALTFGLEVCLAAAGITVVPPLLLEVGVEEKFMTMWLGIG	60	
Qy	61	PVLGLVCVPLLGASDHWRGYGRRRPPIWALSGLILLSFLIPRAGWLAGLCLCPDRPL	120	
Db	61	PVLGLVCVPLLGASDHWRGYGRRRPPIWALSGLILLSFLIPRAGWLAGLCLCPDRPL	120	
Qy	121	ELALLIGVGLDPCGVCFTPLEALLSDLFRDPDHCQAVSVYAFMISLGGCGLYLPA	180	
Db	121	ELALLIGVGLDPCGVCFTPLEALLSDLFRDPDHCQAVSVYAFMISLGGCGLYLPA	180	
Qy	181	IDWDTSAIAPYLGTEECFLGLLTLIFUTCVAATLLVAEEAALGPTEPAEGLSAPLSLPH	240	
Db	181	IDWDTSAIAPYLGTEECFLGLLTLIFUTCVAATLLVAEEAALGPTEPAEGLSAPLSLPH	240	
Qy	241	CCPCRARIAFNLGALLPRLHQLCCRMPTLRLRVFAELCSWMALMTTFLFYDFVGSGL	300	

Db	241	CCPCRBALFRNLGALLPRHLQLCRRMPRTURRLFVABELCSWMLMTTTLFTYDFVGEGL	300
Qy	301	YQGVPRAEPTGEARRHHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA	360
Db	301	YQGVPRAEPTGEARRHHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA	360
Qy	361	APFVAAGATCLSHSVAVVTASAAUTGTFSTASQLITPYTLASLYHREKOVFLPKYRGDTCG	420
Db	361	APFVAAGATCLSHSVAVVTASAAUTGTFSTASQLITPYTLASLYHREKOVFLPKYRGDTCG	420
Qy	421	ASSEDSLMTSFLPGPKPCAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTFA	480
Db	421	ASSEDSLMTSFLPGPKPCAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTFA	480
Qy	481	RVVPGRGICLDLATLDSAFLLSOVAPSLFMGSIIVOLSSQSVTAYMYVSAAGLGVAIYFATQ	540
Db	481	RVVPGRGICLDLATLDSAFLLSOVAPSLFMGSIIVOLSSQSVTAYMYVSAAGLGVAIYFATQ	540
Qy	541	VVFDKSDLAKYSA	553
Db	541	VVFDKSDLAKYSA	553

RESULT 9

```

US-09-895-793-113
; Sequence 113, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITL OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-113

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	Query Match	100.0%	Score 2861;	DB 3;	Length 553;
	Best Local Similarity	100.0%;	Prod. NO. 9.4e-240;		
	Matches 553;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MVORLWSRLRRKQALLVNLITFGLEVCLAAGITVPPLLELVGVGEKFMFMVLGIG	60		
Db	1	MVORLWSRLRRKQALLVNLITFGLEVCLAAGITVPPLLELVGVGEKFMFMVLGIG	60		
Qy	61	PVIGLVCVPLLGASDHWRGYRRRRPTFWALSGILLSLFLIIPRAGWLAGLLCPDRPPL	120		

Db 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLLSLFIPIRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFTPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQEBCLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLPH 240
Db 181 IDWTSALAPYLGTQEBCLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLPH 240
QY 241 CCPCRLAFNLGALLPRHLQCCRMPTLRRLLFVAELCSWMLMTFTLFYDFVGEGL 300
Db 241 CCPCRLAFNLGALLPRHLQCCRMPTLRRLLFVAELCSWMLMTFTLFYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTA 480
Db 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTA 480
QY 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQVTAYMVSAAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 10
US-09-895-814-113
; Sequence 113, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinala de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-895-814-113
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9,4e-240; Mismatches 0; Indels 0; Gaps 0;
Matches 553; Conservative 0;
QY 1 MVQRLWVSRLRHRKAQALLVNLTLFGLVEVCLAAAGITVYVPPLLLEVGVEKEKMTWVLGIG 60
Db 1 MVQRLWVSRLRHRKAQALLVNLTLFGLVEVCLAAAGITVYVPPLLLEVGVEKEKMTWVLGIG 60
QY 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLLSLFIPIRAGWLAGLLCPDRPL 120
Db 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLLSLFIPIRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFTPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQEBCLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLPH 240
Db 181 IDWTSALAPYLGTQEBCLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLPH 240
QY 241 CCPCRLAFNLGALLPRHLQCCRMPTLRRLLFVAELCSWMLMTFTLFYDFVGEGL 300
Db 241 CCPCRLAFNLGALLPRHLQCCRMPTLRRLLFVAELCSWMLMTFTLFYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTA 480
Db 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTA 480
QY 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQVTAYMVSAAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553
RESULT 11
US-10-012-896-113
; Sequence 113, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinala de Bassols, Carlota
; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-113

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLRHRKAQLLVNLITFGLVCLAAAGITYVPPLLEVGVEEKMFTMVLGIG 60
DB 1 MVORLWVSRLLRHRKAQLLVNLITFGLVCLAAAGITYVPPLLEVGVEEKMFTMVLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVGLLDFCQVCFTPLEALLSDFRDPDHCROQVSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLLDFCQVCFTPLEALLSDFRDPDHCROQVSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
DB 181 IDWTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
QY 241 CPCRARLAFRNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
DB 241 CPCRARLAFRNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
QY 361 APVVAAGATCLSHVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APVVAAGATCLSHVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDIALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYIFATQ 540
DB 481 RVVPGRGICLDIALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYIFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 12

US-10-010-940-113
; Sequence 113, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-113

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLRHRKAQLLVNLITFGLVCLAAAGITYVPPLLEVGVEEKMFTMVLGIG 60
DB 1 MVORLWVSRLLRHRKAQLLVNLITFGLVCLAAAGITYVPPLLEVGVEEKMFTMVLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVGLLDFCQVCFTPLEALLSDFRDPDHCROQVSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLLDFCQVCFTPLEALLSDFRDPDHCROQVSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
DB 181 IDWTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
QY 241 CPCRARLAFRNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
DB 241 CPCRARLAFRNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
QY 361 APVVAAGATCLSHVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APVVAAGATCLSHVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDIALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYIFATQ 540
DB 481 RVVPGRGICLDIALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYIFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 13

US-10-144-678A-113
; Sequence 113, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144, 678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: Fast-Seq for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-113

* Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHKAQLLLVNLITFGLVCLAAAGITYVPPLLLEVGVEEKFTMWLGIG 60
DB 1 MVQRLWVSRLLRHKAQLLLVNLITFGLVCLAAAGITYVPPLLLEVGVEEKFTMWLGIG 60

QY 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLIGLLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLIGLLSLFLIPRAGWLAGLLCPDPRPL 120

QY 121 ELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180

QY 181 IDWDT SALAPYLGTQECLFGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
DB 181 IDWDT SALAPYLGTQECLFGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240

QY 241 CCPCRLARLAFRNLGALLPRHLQCCRMPTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
DB 241 CCPCRLARLAFRNLGALLPRHLQCCRMPTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300

QY 301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRTGTRAVYLASVA 360
DB 301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRTGTRAVYLASVA 360

QY 361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420

QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480

QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSI VQLSQSVTAYMVSAAGLGLVAIFYATQ 540
DB 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSI VQLSQSVTAYMVSAAGLGLVAIFYATQ 540

QY 541 VVFDKSDLAKYSA 553
VVFDKSDLAKYSA 553

Db 541 VVFDKSDLAKYSA 553

RESULT 14
US-10-005-907-13
Sequence 13, Application US/10005907
Publication No. US20030166881A1
GENERAL INFORMATION:
APPLICANT: Union Chimique Beige, S.A.
APPLICANT: No. US20030166881A1ka, Karl
APPLICANT: Pirozzi, Gregory
APPLICANT: Einstein, Richard
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST C
TITLE OF INVENTION: ACTIVATION
FILE REFERENCE: 053529-5005
CURRENT APPLICATION NUMBER: US/10/005,907
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-10-005-907-13

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHKAQLLLVNLITFGLVCLAAAGITYVPPLLLEVGVEEKFTMWLGIG 60
DB 1 MVQRLWVSRLLRHKAQLLLVNLITFGLVCLAAAGITYVPPLLLEVGVEEKFTMWLGIG 60

QY 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLIGLLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVGLVCVPLLGASDHWGRYGRRRPFIWALSGLIGLLSLFLIPRAGWLAGLLCPDPRPL 120

QY 121 ELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180

QY 181 IDWDT SALAPYLGTQECLFGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
DB 181 IDWDT SALAPYLGTQECLFGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240

QY 241 CCPCRLARLAFRNLGALLPRHLQCCRMPTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
DB 241 CCPCRLARLAFRNLGALLPRHLQCCRMPTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300

QY 301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRTGTRAVYLASVA 360
DB 301 YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRTGTRAVYLASVA 360

QY 361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APFVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420

QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480

QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSI VQLSQSVTAYMVSAAGLGLVAIFYATQ 540
DB 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSI VQLSQSVTAYMVSAAGLGLVAIFYATQ 540

QY 541 VVFDKSDLAKYSA 553
VVFDKSDLAKYSA 553

RESULT 15
US-10-294-025-113
Sequence 113, Application US/10294025

```
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kaos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-294-025-113

Query Match      100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MVORLWVSRLRRKKAQLLLVNLITFGLVCLAAAGITYVPPLLLEVGVEEKFTMTVLGIG 60
Db      1  MVORLWVSRLRRKKAQLLLVNLITFGLVCLAAAGITYVPPLLLEVGVEEKFTMTVLGIG 60
QY      61  PVGLGVCVPLLGASDHWGRGRRRPFITWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
Db      61  PVGLGVCVPLLGASDHWGRGRRRPFITWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
QY      121 ELALLIGVGLLDFCGQVCFPTPLEALLSDFRDPDHCRQAYSYYAFMISLGGCLGYLLPA 180
Db      121 ELALLIGVGLLDFCGQVCFPTPLEALLSDFRDPDHCRQAYSYYAFMISLGGCLGYLLPA 180
QY      181 IDWDTAALAPYLQTQBECLFGLLTILFTCTVAATLLVABEAAALGPTPEAEGLSAPLSPH 240
Db      181 IDWDTAALAPYLQTQBECLFGLLTILFTCTVAATLLVABEAAALGPTPEAEGLSAPLSPH 240
QY      241 CCPCRLARLAFRNIGALLPRHLQCCRMPTRLRELFAVELCSWMAALMTFTLFYTDVFVGEGL 300
Db      241 CCPCRLARLAFRNIGALLPRHLQCCRMPTRLRELFAVELCSWMAALMTFTLFYTDVFVGEGL 300
QY      301 YQGVPRAEPTGEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
Db      301 YQGVPRAEPTGEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
QY      361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db      361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY      421 ASSEDSIMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db      421 ASSEDSIMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY      481 RVVPGRGICLDLAILDSAFLLSQVAFSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
Db      481 RVVPGRGICLDLAILDSAFLLSQVAFSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY      541 VVFDKSDLAKYSA 553
Db      541 VVFDKSDLAKYSA 553
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Job time : 185 secs

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OM protein - protein search, using sw model

Run on: May 27, 2006, 04:06:44 ; Search time 15 Seconds
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Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQLWVSLRRHRAQLL.....AIVFATQVVDKSLAKYSA 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
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2: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
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8: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	323.5	11.3	507	US-10-953-349-4710	Sequence 4710, Ap
2	323.5	11.3	512	US-10-953-349-4709	Sequence 4709, Ap
3	313	10.9	511	US-10-953-349-13600	Sequence 13600, A
4	312	10.9	475	US-10-953-349-13601	Sequence 13601, A
5	274.5	9.6	434	US-10-953-349-4711	Sequence 4711, Ap
6	177	6.2	351	US-10-953-349-13602	Sequence 13602, A
7	129	4.5	240	US-10-953-349-18828	Sequence 18828, A
8	126	4.4	228	US-10-953-349-18830	Sequence 18830, A
9	126	4.4	230	US-10-953-349-18829	Sequence 18829, A
10	113	3.9	1403	US-10-505-928-471	Sequence 471, App
11	103.5	3.6	537	US-10-953-349-31157	Sequence 31157, A
12	103.5	3.6	550	US-10-953-349-31156	Sequence 31156, A
13	103.5	3.6	584	US-10-953-349-31155	Sequence 31155, A
14	100	3.5	342	US-10-953-349-33245	Sequence 33245, A
15	99	3.5	443	US-10-953-349-37180	Sequence 37180, A
16	97.5	3.4	245	US-10-953-349-26339	Sequence 26339, A
17	95.5	3.3	1443	US-11-293-697-3844	Sequence 3844, Ap
18	93.5	3.3	442	US-10-953-349-2567	Sequence 2567, Ap
19	93.5	3.3	489	US-10-953-349-2566	Sequence 2566, Ap
20	92.5	3.2	391	US-10-953-349-37182	Sequence 37182, A
21	92.5	3.2	416	US-10-953-349-37181	Sequence 37181, A
22	92	3.2	403	US-10-953-349-5592	Sequence 5592, Ap
23	91	3.2	424	US-10-953-349-11588	Sequence 11588, A
24	91	3.2	460	US-10-953-349-11587	Sequence 11587, A
25	91	3.2	486	US-10-953-349-11586	Sequence 11586, A

ALIGNMENTS

RESULT 1

US-10-953-349-4710
; Sequence 4710, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4710
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4710

Query Match 11.3%; Score 323.5; DB 6; Length 507;
Best Local Similarity 24.1%; Pred. No. 86-20;
Matches 123; Conservative 92; Mismatches 195; Indels 101; Gaps 18;

QY	14	RKAQLLVNLLTFGLVCLAAAGITYVPPLLLBVGVEEKFMVVLGIGPVGLVCVPLLGS	73	Sequence 41, Appli
Db	23	RURKIISVSSIAAGVQFGWALQLSLTPVQLLGIPIHKWASLIWLCGPISGMLVQPIVGY	82	Sequence 3, Appli
QY	74	ASDHWGRYGRRRPPTWALSGLISLFLIPRAGWAGL-----LCPDPRPLEALLI	126	Sequence 14, Appli
Db	83	HSDRCTSRFRRRPPIVAGAGVTVAVFLI---GYAADIGHSMGDOGLDKPKPTAIFA	139	Sequence 27707, A
QY	127	LGVLGLDFGQVCFPTPLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL	178	Sequence 27706, A
Db	140	LGFWILDVANNTLQGPCRAFLADLSAGNAKKTETANAFSPFMAVGNVLGYAAGSYENLY	199	Sequence 27705, A
QY	179	PAIDWD-TSALAPYLGTOBECIFGLTLTLPFCVAATLLVABEAAAGPTPEBGLSAPSL	237	Sequence 2568, Ap
Db	200	KVVPFTMTSCDLYCANLKTCCFLSITLL-LIVTFVSLCYVKEKPMTPPTADGKA----	254	Sequence 2567, Ap
QY	238	SHPCPCRARLAFRLNIGALLPRHLQCCRPRTLRLFVAELCSWMLMTFTLFYDFVG	297	Sequence 36059, A
Db	255	-----SNVPF--FGEIFGAFKEL-----KRPMMMLLIVTALNWTANFPFLFDFTDMWG	300	Sequence 3831, Ap
QY	298	EGLYQGVPAEPGCTEARRHYDEGVRMGSLGLFQCAISLVFSLVMDRLVQRFCTRAVYLA	357	Sequence 31943, A
Db	301	REVYGNSDATATASKLYNDGVRAGALGLMLNAIVLGMFMSLGVENIGRKLIG-GAKRLW	359	Sequence 28815, A
QY	358	SVAAPFPAAGATCLSHSVAV-----VTASA-----ALTG-----FT	388	Sequence 31944, A

Query Match 10.9%; Score 312; DB 6; Length 475;
Best Local Similarity 24.3%; Pred. No. 6.8e-19;
Matches 141; Conservative 77; Mismatches 205; Indels 158; Gaps 23;
QY 18 LLLVNLTFGLVCLAAAGTVPPLLEVGVEEKFMTVMVLGIGPVLGVCVPLGSGASDH 77
DB 1 MFVASIAAGIQFQWALQSLTTPYVQLLGVPHAAASFWLWVQVPIVGYSDH 60
QY 78 WRGRRRRPFIWALSIGILLSLFLIPRA---GWLAG-LCCPDRPLEALLILGVGLLD 133
DB 61 CTSRFRGRRPFIWALSIGILLSLFLIPRA---GWLAG-LCCPDRPLEALLILGVGLLD 133
QY 134 FCQVCFPLEALLSLDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LLPAID 182
DB 121 VANMLGQPCRAFLADLAGDQKRIANGFFSFMVAVGNVLGYAAGSYKGLHMKFPFT- 179
QY 183 WDTLSALAPYLGTQEECLFGLLTFLITCVAAATLLVAEEAALGPTBPAEGLSAPSLPHC 241
DB 180 -ETKACDVCANLKSCFFSILLLLFLATVA--LLYVKQKV-----EARALD-DATQPS 231
QY 242 CPCRLAFRNGLALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLYDFVGEGLY 301
DB 232 -----FPFLSALKEL-----KRPMMMLVTVAVNWGVWFFYFLFDTDMGREVY 276
QY 302 QGVPRAPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRL-----VQR- 348
DB 277 GG-----QVGEDA---YANGVRVSGSLGLMNAVNLVGFMSLAVEPLGKMGVGVKRLVAIVNF 329
QY 349 -----FGTRAVLASVAAPVAAAGATCLSH-SVAVVTASAALTG-----FTFSALQIL 395
DB 330 ILAIGFG-MTVVITKVAEHQKKNPAAGVHPSEGVVGVVGVVGLVGPVLAITFS-----V 384
QY 396 PYTLASLYHREKQVFLPKYRGDTGGASSEDLSMTSFLPGKPGAPFNGHVGAGGSLLP 455
DB 385 PFALAGSIY----- 392
QY 456 PPALCGACACDVSRVNVGCEPTEARVVPGRGICLDLILDSAFLLSQVAPSLFMSIVQ 515
DB 393 -----CSAS-----GAGQGLSLGLVNLAIIVVPMVSTLSGFWD 427
QY 516 L--SQSVTAYMVSAGLGLVAIVFATQVVPDK--SDLAKYSA 553
DB 428 LFGGGLNLPFWMGVAANAALSAIMAILVLLPTPKPADEAKASS 468

RESULT 5
US-10-953-349-4711
; Sequence 4711, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4711
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4711

Query Match 9.6%; Score 274.5; DB 6; Length 434;
Best Local Similarity 24.8%; Pred. No. 8.2e-16;
Matches 113; Conservative 72; Mismatches 170; Indels 101; Gaps 18;
QY 69 PLLGSASDHWGRGRRRPFIIWALSIGILLSLFLIPRAGWLAGL-----LCPDRPL 121
DB 5 PIVGYHSDRCTSRFRGRRRPFIVAGAGLVTVAVFLI---GYAADIGHSMGQDLDKPKKTRA 61
QY 122 LALLILGVGLDFCGQVCFPLEALLSLDLFR-DPDHCRQAYSVYAFMISLGGCLGY---- 176
DB 62 IIAIFALGFWILDVANNTLOGPCRAFLADLSAGNAKTRTANAFFSFFMAGVNVGLGYAAGS 121
QY 177 ----LLPAIDWD-TSALAPYLGTQEECLFGLLTFLITCVAAATLLVAEEAALGPTBPAEGL 232
DB 122 YRNLYKVPFTWTESCDLYCANLKTCFFLSITLL-LIVTFVSLCYVKEKWPWTPEPTADGK 180
QY 233 SAPSLSPHCCPCRLAFRNGLALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLY 232
DB 181 A-----SNVPF--FGEIFGAFKEL-----KRPMMMLIIVTALNMIAWFFPFLFD 222
QY 293 TDFVGEGLYQGVPRAPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTR 352
DB 223 TDMGREVYVGNSSDATATAASKLYNDGVRAGALGLMNAIVLGFMSLGVWIGRKLKLG-G 281
QY 353 AVYLASVAAPVAAAGATCLSHSVAV-----VTASA-----ALTG- 386
DB 282 AKRLWGINVNFIL---AICLAMTVVTKQAEHRRDHGGAKTGPPGNVTAGALTFLAILGI 338
QY 387 ---FTFSALQIILPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTS 430
DB 339 POAITFS-----IPFALASIFSTNSGAGQGLSLGLVNLAIIVVPMVSVGGPFDLFGGG 384
QY 431 FLPGPKPGAPFNGHVGAGGSGLL-----PPPPA 459
DB 395 NIPA-----FVLGAIAAAVSGVLALTVLPSPPDA 424

RESULT 6

US-10-953-349-13602
; Sequence 13602, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 13602
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13602

Query Match 6.2%; Score 177; DB 6; Length 351;
Best Local Similarity 23.2%; Pred. No. 8.9e-08;
Matches 105; Conservative 49; Mismatches 145; Indels 154; Gaps 21;
QY 142 PLEALLSLDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LLPAIDWDTSALAP 190
DB 5 PCRAFLADLAGDQKRIANGFFSFMVAVGNVLGYAAGSYKGLHMKFPFT--ETKACDV 62
QY 191 YLGTQEECLFGLLTFLITCVAAATLLVAEEAALGPTBPAEGLSAPSLPHCCPCRLA 249
DB 63 FCANLKSCFFSILLLLFLATVA--LLYVKQKV-----EARALD-DATQPS----- 107
QY 250 FRNLGALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLYDFVGEGLYQGVPRAP 309
DB 108 FFQLFSALKEL-----KRPMMMLVTVAVNWGVWFFYFLFDTDMGREVYGG-----QV 156
QY 310 GTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRL-----VQR-----FGT 351

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; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18828
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18828

Query Match      4.5%; Score 129; DB 6; Length 240;
Best Local Similarity 22.5%; Pred. No. 0.00058;
Matches 71; Conservative 33; Mismatches 94; Indels 118; Gaps 12;

QY 267 MPTLRRLFVAELCSWMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGL 326
DB 7 LKRPMMMLMTAVNVWGWFPYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGL 59
QY 327 GLFLOCAISLVFSLVMDRL-----VQR-----FGTRAVVYLASVAAPFVAAGA 368
DB 60 GLMNVAVVGLFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMN 118
QY 369 TGLSLH-SVAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 119 AAVGHPSEGVVGVSMVFFGLVPLAITFS---VPPALASIY----- 157
QY 421 ASSDSLMTSLFLPGKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPT 480
DB 158 -----CSAS----- 161
QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 538
DB 162 ----GAGQGLSLGLNLAIWVPMVSTLSGPDALFGGGLNLPAPMVGAAAAAISAINAI 217
QY 539 TQVVFDPK-SDLAKYSA 553
DB 218 VLLPTPKPADEAKASS 233

RESULT 8
US-10-953-349-18830
; Sequence 18830, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18828
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18828

Query Match      4.5%; Score 129; DB 6; Length 240;
Best Local Similarity 22.5%; Pred. No. 0.00058;
Matches 71; Conservative 33; Mismatches 94; Indels 118; Gaps 12;

QY 267 MPTLRRLFVAELCSWMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGL 326
DB 7 LKRPMMMLMTAVNVWGWFPYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGL 59
QY 327 GLFLOCAISLVFSLVMDRL-----VQR-----FGTRAVVYLASVAAPFVAAGA 368
DB 60 GLMNVAVVGLFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMN 118
QY 369 TGLSLH-SVAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 119 AAVGHPSEGVVGVSMVFFGLVPLAITFS---VPPALASIY----- 157
QY 421 ASSDSLMTSLFLPGKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPT 480
DB 158 -----CSAS----- 161
QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 538
DB 162 ----GAGQGLSLGLNLAIWVPMVSTLSGPDALFGGGLNLPAPMVGAAAAAISAINAI 217
QY 539 TQVVFDPK-SDLAKYSA 553
DB 218 VLLPTPKPADEAKASS 233

RESULT 9
US-10-953-349-18829
; Sequence 18829, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18829
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18829

Query Match      4.4%; Score 126; DB 6; Length 230;
Best Local Similarity 22.7%; Pred. No. 0.00099;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSWMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 4 LMLVTAVNVWGWFPYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLMNVAV 56
QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVYLASVAAPFVAAGATCLSH-S 374
DB 57 VLGFMMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 115
```

```

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18830
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18830

Query Match      4.4%; Score 126; DB 6; Length 228;
Best Local Similarity 22.7%; Pred. No. 0.00098;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSWMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 2 LMLVTAVNVWGWFPYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLMNVAV 54
QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVYLASVAAPFVAAGATCLSH-S 374
DB 55 VLGFMMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 113
QY 375 VAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSED 427
DB 114 EGVVGVSMVFFGLVPLAITFS---VPPALASIY----- 145
QY 428 MTSFLPGKPGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPT 487
DB 146 -----CSAS----- 152
QY 488 ICLELAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 545
DB 153 OGLSLGLNLAIWVPMVSTLSGPDALFGGGLNLPAPMVGAAAAAISAINAILLPTPK 212
QY 546 -SDLAKYSA 553
DB 213 PADEAKASS 221

RESULT 9
US-10-953-349-18829
; Sequence 18829, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18829
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18829

Query Match      4.4%; Score 126; DB 6; Length 230;
Best Local Similarity 22.7%; Pred. No. 0.00099;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSWMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 4 LMLVTAVNVWGWFPYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLMNVAV 56
QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVYLASVAAPFVAAGATCLSH-S 374
DB 57 VLGFMMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 115
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Qy	375	VAVVTASAAALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSDSL	427
		: :	
Db	116	EGVVGVSMVFVGVLGVPALITFS-----VFFALASIY	147
		: :	
Qy	428	MTSFLPGPKCAPFPNGHVAGGSGLLPPPALCGASACDVSVRVVVVGPETEARVVVPGKG	487
		: :	
Db	148	-----CSAS-----	GAG 154
		: :	
Qy	488	ICLDLAILDASFLLSQVAPSLFMSIVOL--SQSVTAYVMWSAAGLGLVAIYPATQVFDK	545
		: :	
Db	155	OQLSLGVNLTAIVVPMQVMMVSTLSGPDWDLFGGGLNLPAFMVGAAAAALSAINAIUVLLPTPK	214
		: :	
Qy	546	-SDLAKSYA 553	
		: :	
Db	215	PDEAKASS 223	
		: :	
RESULT 10			
US	10-505-928-471		
:	Sequence 471, Application US/10505928		
:	Publication No. US20060088532A1		
:	GENERAL INFORMATION:		
:	APPLICANT: Ludwig Institute for Cancer Research et al.		
:	TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES		
:	FILE REFERENCE: 28967/39178		
:	CURRENT APPLICATION NUMBER: US/10/505,928		
:	CURRENT FILING DATE: 2004-08-27		
:	PRIOR APPLICATION NUMBER: US 60/363,019		
:	PRIOR FILING DATE: 2002-03-07		
:	NUMBER OF SEQ ID NOS: 866		
:	SOFTWARE: PatentIn 3.2		
:	SEQ ID NO 471		
:	LENGTH: 1403		
:	TYPE: PRT		
:	ORGANISM: Homo sapiens		
US	10-505-928-471		

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Qy      429 TSFLPG 434
      |
      ||
Db      1254 HSDNPG 1259

RESULT 11
US-10-953-349-31157
; Sequence 31157, Application US/109533349
; Publication No, US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLY-
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31157
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31157

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RESULT 12
US-10-953-349-31156
; Sequence 31156, Application US/10953349

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 03:59:53 ; Search time 42 Seconds
(without alignments)
1266.854 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLRRHKAQLLL.....AIYFATQVVFDSKLAKYSA 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length	Description
1	347.5	12.1	515 2 T14340 sucrose-proton tra
2	337.5	11.8	523 2 T12198 sucrose transport
3	330	11.5	516 2 JQ2389 sucrose transport
4	328.5	11.5	594 2 G84441 probable sucrose-p
5	324.5	11.3	525 2 S28052 sucrose transport
6	323.5	11.3	512 2 G86360 probable sucrose-p
7	323.5	11.3	512 2 S38196 sucrose transport
8	317.5	11.1	507 2 S48789 sucrose transport
9	311	10.9	533 2 S43142 sucrose transport
10	305.5	10.7	501 2 T14339 sucrose-proton tra
11	297.5	10.4	428 2 S48788 sucrose transport
12	294	10.3	510 2 S38657 sucrose transport
13	294	10.3	523 2 S51114 sucrose-proton sym
14	292.5	10.2	512 2 F96741 probable sucrose t
15	282	10.2	537 2 T02982 probable sucrose t
16	286	10.0	474 2 A86234 hypothetical prote
17	281.5	9.8	491 2 E96691 probable sucrose-p
18	279.5	9.8	513 2 S38197 sucrose transport
19	276.5	9.7	492 2 A84520 probable sucrose-p
20	273	9.5	503 2 S52377 sucrose transport
21	235.5	8.2	553 2 T38541 probable sucrose c
22	191	6.7	452 2 F75217 hypothetical prote
23	187.5	6.6	541 2 B87532 transporter, proba
24	142	5.0	544 2 S75696 melibiose carrier
25	139.5	4.9	454 2 A75444 hypothetical prote
26	138.5	4.8	430 2 E75217 transporter P8217
27	136	4.8	418 2 B87536 membrane protein,
28	133	4.6	389 2 G83413 probable MFS trans
29	128.5	4.5	422 2 G83503 probable MFS trans

30	128.5	4.5	594	2	A83096	probable permease
31	127.5	4.5	472	2	E82639	resistance protein
32	127	4.4	451	2	E81781	probable integral
33	126	4.4	394	2	A83073	tetracycline resis
34	126	4.4	394	2	G98213	drug efflux protei
35	126	4.4	451	2	A81206	sugar transporter,
36	125.5	4.4	399	2	JQ1479	tetracycline resis
37	125	4.4	391	2	S74688	hypothetical prote
38	125	4.4	407	2	H75515	tetracycline-efflu
39	124.5	4.4	399	1	S38656	tetA protein - Pse
40	123.5	4.3	400	2	AG2866	MFS permease (drug
41	123.5	4.3	400	2	D97643	probable efflux pr
42	123	4.3	440	2	AD0986	hypothetical metab
43	121.5	4.2	398	2	C90349	multidrug-efflux t
44	121.5	4.2	503	2	S43017	puromycin resistan
45	121	4.2	483	2	AF2363	hypothetical prote

ALIGNMENTS

RESULT 1

T14340

sucrose-proton transport protein - carrot

N;Alternate names: sucrose/H+ symporter protein

C:Species: Daucus carota (carrot)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T14340

R:Shakya, R.; Sturm, A.

Plant Physiol. 118, 1473-1480, 1998

A:Title: Characterization of source- and sink-specific sucrose/H+ symporters from carrot

A:Reference number: Z17991; MUID:99063785; PMID:9847123

A:Accession: T14340

A>Status: Preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-515 <SHA>

A:Cross-references: UNIPROT:O65803; UNIPARC:UPI0000009CB5F; EMBL:Y16768; NID:g2969883; P

A:Experimental source: cultivar Nantaise; root

C:Genetics:

A:Note: SUT2

C:Superfamily: common tobacco sucrose transport protein

Query Match 12.1%; Score 347.5; DB 2; Length 515;

Best Local Similarity 25.9%; Pred. No. 1.7e-18;

Matches 131; Conservative 80; Mismatches 215; Indels 79; Gaps 17;

QY 17 QLLVNLTFGLEVCLAAGITVPPLLELVGVVEKEFTMVLGIGVGLVCVPLLGASD 76

DB 34 KLVLVAATAAGVQFGWALQSLTTPYVQLGIPHKWAAYIWLCPISGMLVQPIVGYSD 93

QY 77 HWRGRRRPTIWAISLILSLFLIPRAGLAGL-----LCPDRPLELALLILGV 129

DB 94 HQCSFGRRRPIASGAGCAISVILI---GFAADISYKAGDDMSKTLKPRATVTVIGF 150

QY 130 GLLDFCGQVCTFPLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL 178

DB 151 WILDVANMLQGPCRALLADLCSGDTRRMRSAFYSPFMAVGNILGYAAGSYNNLYKLF 210

QY 179 PAIDWDTSLAPYLGTOECLGLTLTFLTCVAATLLVAEEAALGPTPEAGLSAPLS 238

DB 211 PFS--KTHACDLYCANLSCFIISIALLIITVVALSVVRENS--GPPDADAEEP--- 263

QY 239 PHCCPCFARLAPRNLGALLPRHLQCCMRPRTLRLRFLVAELCSWMALMTFTLYTDFVGE 298

264	----	PSSGKIPV--FGELLGALKDL----	PRMILLLLIIVTCLNWIWIAFFFIIFDIDMGR	313
299	GLYQGVPRAPGPTERRHYDEGRVMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLAS	358		
314	EIYGGT--AGQG----	KLYDQGVRAAGLGLLNSVVLGTSIAVEYLVRAVGSGVKI-LWG	366	
359	VAAFPVAAGATCL-----	SHSV-----AVTASA-----	ALTGTFPSALQTL 395	
367	FVNFIATGLVMTVVVSVKVAQHREHSANGQLLPPSAGVKAGALSLSFSLIGIPLSITYSI	426		

Tue May 30 15:28:26 2006

[illegible]

RESULT 3
JQ2389
sucrose transport protein - potato

C:Species: Solanum tuberosum (potato)
C:date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JQ2389; S40310
R:Riesmeier, J.W.; Hirner, B.; Frommer, W.B.
Plant Cell 5, 1591-1598, 1993
A:title: Potato sucrose transporter expression in minor veins indicates a role in phloem
A:Reference number: JQ2389; MUID:94146554; PMID:8312741
A:Accession: JQ2389
A:Molecule type: mRNA
A:Residues: 1-516 <R1E>
A:Cross-references: UNIPROT:Q43653; UNIPARC:UPI000009FF9P; EMBL:X69165; NID:9439293; P11
A:Experimental source: cv. Desiree
C:Comment: The gene encoding for this protein is highly expressed in mature leaves.
C:Superfamily: common tobacco sucrose transport protein
C:Keywords: glycoprotein; transmembrane protein
F:31-53/Domain: transmembrane #status predicted <TM1>
F:67-86/Domain: transmembrane #status predicted <TM2>
F:103-122/Domain: transmembrane #status predicted <TM3>
F:141-160/Domain: transmembrane #status predicted <TM4>
F:180-200/Domain: transmembrane #status predicted <TM5>
F:226-248/Domain: transmembrane #status predicted <TM6>
F:285-304/Domain: transmembrane #status predicted <TM7>
F:331-349/Domain: transmembrane #status predicted <TM8>
F:366-385/Domain: transmembrane #status predicted <TM9>
F:409-427/Domain: transmembrane #status predicted <TM10>
F:429-448/Domain: transmembrane #status predicted <TM11>
F:3.92/Binding site: carbohydrate (Asn) #status predicted

	Query Match	11.5%	Score 330;	DB 2;	Length 516;	
	Best Local Similarity	24.7%	Pred. No. 3,4e-17;			
	Matches 132;	Conservative	93;	Mismatches 197;	Indels 112; Gaps 21;	
QY	4	RLWVSRLRHKQAQLLVNLT	TEGLVCLAA	GYVPP	LLLEVGVEKFTMVLGIGPVL 63	
DB	29	KLM-----	KIIVVASIAG	QFGWALQ	LSLTPYQLLGIPHKFASFWLGGPIS 78	
QY	64	GLVCPVLGASDHWGRYGR	RRPF	IWALSIG	LLSLLFLIPRAGWLAGL-----LCPD 116	
DB	79	GMIQPVVGVYDNCSS	RRFRRPF	IAAGAA	LVMIAVFLI---GFAADLGHASGDTLGKG 135	
QY	117	PRPLEALLILGVCLDF	CCQVCF	TPLEALL	SDLFRDPD-HCROAYSVYAFMISLGGCLG 175	
DB	136	FKPRAIAVVFVGVWIL	VANNM	LOGPCRAL	LADLSGGKSGEMRTANAFFSFFMAVGNILG 195	
QY	176	YLLPAIDW-----	DTSALAP	YLGTE	ECFLF-GLLTFLPFTCVANTLLVAEE-AALGP 225	
DB	196	YAAGSYSHLFKVPFS	TKACDMY	CANLKS	CFFFIAIFLLLSLTITIALTLVRENELPEKDE 255	
QY	226	TEPAEGLSAPLSLPH	CCPCAR	LAFNIG	LALLPRLHOLCCMRPTRLRLFVAELCSWMAL 285	
DB	256	QEIDEKLAGAG-----	SSKVPF	-FGEIF	GALKEL-----PRPMILLVLTCLNIAW 301	
QY	286	MTFTFLFYTD	FGEGLYQ	GVPRAE	EGTEARRHYDEGVRMGSGLGLFQCAISLVFLMDRL 345	
DB	302	FPFFLYD	TDWAKE	VEFG-----	QVGD--ARLYDLGVAGAMGLLQSVVLGFMSLGVBEFL 355	
QY	346	VORFQTRAVYL	ASVAA	FPVAAG	ATCLSHSVAV-----TASAALTGT----- 388	
DB	356	GKKIG-GAKRL	WGILNF	VL---A	ICLAWTILVTWAKESRQHDPA	GLTGMFTPGVKIGAL 411
QY	389	--FSALQI-----	LPYTLAS	LYHREX-----	OVFLPKYRGDTGGGASSED 426	
DB	412	LLFAALGIP	PLAATFS	IPFALAS	IFSSNRGSGQLSLGVNLAI	VVVFQMLVLVGGFWDDL 471
QY	427	LMTSLDPG	KPGCAF	PNNGH	VGAGSG-----LLPPPPAL	CGASACDVSVRVVVG 475
DB	472	FGGNGLPG-----	FWGAV	AAAA	SAVALTWL	TFSPFA-----DAKPAVAMG 512

RESULT 4
G84441
probable sucrose-proton symporter [imported] - *Arabidopsis thaliana*
C. Section: *Arabidopsis thaliana* (mouse-ear cress)

A;Cross-references: UNIPROT:Q03411; UNIPARC:UIP000001361132; EMBL:X67125; NID:g21318; PDB:
C;Superfamily: common tobacco sucrose transport protein
C;Keywords: transmembrane protein

Query Match 11.3%; Score 324.5; DB 2; Length 525;
Best Local Similarity 23.2%; Pred.No.9.le-17;
Matches 129; Conservative 91; Mismatches 196; Indels 141; Gaps 20;

QY 23 LITFGLEVLCAAGITY-----VPLLLLEVGVBEKPMTMVLGIGFVLGLVCVPILGSA 74
| | | | | : : : : :
Db 35 LKKLGILVASAAGVGQFMALQLSLTPYVQLLGIPTHTWAAYIWLCCGPISGMIVQPLVGY 94
| | | | | : : : : :
QY 75 SDHWGRYGRRRPFPIWALSIGILLSLFLPRAGWLA--GLLCDDP-----RPLELALLIL 127
| | | | | : : : : :
Db 95 SDRCTSRFRRRPFIAAGAALVAVALGLI---GFAADIGAASGDPTGNVAKPRAIAVFVV 151
| | | | | : : : : :
QY 128 GVCLDFCGQCVFTPLEALLSDLFR--DPDHCROAYSVAFMISLGCLGVLPAID---- 182
| | | | | : : : : :
Db 152 GFWILDVANNTLGGPCRALLDMAAGSQTKTRYANAFFSFFMALGINIGGYAAGYSRLYT 211
| | | | | : : : : :
QY 183 ----WDTSALAPYLGTQEELFCGLLT-LIFLTCAAATLLVAEEAALGPTPEAGLSAPS 237
| | | | | : : : : :
Db 212 VFPTKTAAADVCANLKSCFFISITLLVITLILSVVKERQITIDEIQEEDLKNRN 271
| | | | | : : : : :
QY 238 SPHCCPCRARLARFNIGALLPRHLQCCMRPTLRRLFVAELCSWMALMTFTLYFYTFVG 297
| | | | | : : : : :
Db 272 SSGC-----ARLPF--FGQLIGALKDL----PKPMLTLLLVTLNWTIANWPFFLLFDTDWG 321
| | | | | : : : : :
QY 298 EGLYQGVPAEPGTEARRHYDEGRVMSGLGFLOCAISLVFSVMDDLVRQFG--TRAVY 355
| | | | | : : : : :
Db 322 KEYVGT-----VGBGKLYDGQVHAGALGLMINSVVLGVMSLSTEGLMRVGGAKRLWG 375
| | | | | : : : : :
QY 356 LASVAAPPVAAGATCLSHSVAVVTASAALTGTFTSALQILPYTLASLYHREKQVFLPKYR 415
| | | | | : : : : :
Db 376 IVNIIL-----AVCLAMTV-LVTKSAE-----HFDSHHIM---- 405
| | | | | : : : : :
QY 416 GDTGGASSDSLWTSFLPGKPFPNGPHGVGAGSGLLPPPPPACGASACDVSVRVVVG 475
| | | | | : : : : :
Db 406 -----GSAPVPPPPA--GVKGGAALAIFAVLG 429
| | | | | : : : : :
QY 476 EPTEARV-VP-----GRGICLDIALDSAFLLSQV-----AP 506
| | | | | : : : : :
Db 430 IPLAITSPFPALASIFSASSGGSLGLVNLAIVPQMFVSVTSGPWDMFGGNNLP 489
| | | | | : : : : :
QY 507 SLFMGSIIVQLSSQVTA 523
| | | | | : : : : :
Db 490 AFVVGVAATAASAVLSF 506
| | | | | : : : : :

RESULT 6
G86360
probable sucrose-proton symporter SUC2 protein T22J18.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86360
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: AB6141; PMID:21016719; PMID:11130712
A;Accession: G86360
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
A;Cross-references: UNIPROT:Q80550; UNIPARC:UIP00000482AD; GB:AE005172; NID:g3287697; P:
C;Genetics:
A;Map position: 1

C:Superfamily: common tobacco sucrose transport protein

Query Match 11.3%; Score 323.5; DB 2; Length 512;
Best Local Similarity 24.1%; Pred. No. 1e-16;
Matches 123; Conservative 92; Mismatches 195; Indels 101; Gaps 18;

QY 14 RKAQLLVNLTTFGLEVCLAAGITYVPPLLEVGVEEKFTMTVLGIGPVGLVCVPLLGS 73
DB 28 RLKRIISVSSIAAGVQFGWALQSLLTPVQLLGIPIHKWASLIWLCGPISGMVQPIVGY 87

QY 74 ASDHWRGRRRPRPIWALSGLILLSLELI PRAGWLAGL-----LCPDPRPLELALLI 126
DB 88 HSDRCTSRFRRRPRPIVAGAGLVTVAVFLI---GYAADIGHSMGQDQPKPKTRAIAPA 144

QY 127 LGVGLLDFCGQVCFPLEALLSDLFR-DPDHCRQAYSVAFMISLGGCLGY-----LL 178
DB 145 LGFWILDVANNTLQGPCRAFLADLSAGNAKKTRTANAFSPFPMAGNVLYGAAGSYRNLY 204

QY 179 PAIDWD-TSALAPYLGTOECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPSL 237
DB 205 KVPFTMTSCDLYCANLKTCCFLSITLL-LIVTFVSLCYVKEKPTPEPTADGKA---- 259

QY 238 SHPCPCRARLAFRNLGALLPRHLQCCRMPTLRFLVAELCSNMALMTFTLFTDFVG 297
DB 260 -----SNVPF--FGEIFGAFKEL-----KRPMMMLLIIVTALNWIAPFLLFDTDMWG 305

QY 298 EGLYQGVPRAPGTEARRHYDEGVRMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLA 357
DB 306 REVYGGNSDATATAASKLYNDGVRAGALGLMNAIVLGFMSLGVWEIGRKLK-GAKRLW 364

QY 358 SVAAPFVAAGATCLSHSVAV-----VTASA---ALTG---FT 388
DB 365 GIVNFIL--AICLAMTVVTVTKQAENHRDHGAKTGPNGVNTAGALTTLFAILGIPQAIT 421

QY 389 FSALQLPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTSFLPGP 435
DB 422 FS-----IPFALASIFSTNSGAGGSLGLVNLAIIVPQMWISVGGGPFDELFGGNIPA- 476

QY 436 KPGAPFNGHVAGGSGLL-----PPPPA 459
DB 477 -----FVLGAIAAASVGLALTVLPSPPDA 502

RESULT 7
S38196
sucrose transport protein SUC2 - Arabidopsis thaliana
N:Alternate names: sucrose-proton symporter SUC2
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S38196; T00773
R:Sauer, N.K.
submitted to the EMBL Data Library, October 1993
A:Description: SUC1 and SUC2: two sucrose transporters from Arabidopsis thaliana.
A:Reference number: S38196
A:Accession: S38196
A:Molecule type: mRNA
A:Residues: 1-512 <SAU>
A:Cross-references: UNIPROT:Q39231; UNIPARC:UPI0000049ABE; EMBL:X75382; NID:g407091; PID:R/Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence.
A:Reference number: Z14202
A:Accession: T00773
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-490, 'A', 492-512 <VYS>
A:Cross-references: UNIPARC:UPI00000482AD; EMBL:AC003979; NID:g3172156; PID:g3287687; GS A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: SUC2; ATSP:T22J18.12
A:Map position: 1
A:Introns: 419/3; 441/1; 455/3

C:Superfamily: common tobacco sucrose transport protein
C:Keywords: sugar transport

Query Match 11.3%; Score 323.5; DB 2; Length 512;
Best Local Similarity 24.1%; Pred. No. 1e-16;
Matches 123; Conservative 92; Mismatches 195; Indels 101; Gaps 18;

QY 14 RKAQLLVNLTTFGLEVCLAAGITYVPPLLEVGVEEKFTMTVLGIGPVGLVCVPLLGS 73
DB 28 RLKRIISVSSIAAGVQFGWALQSLLTPVQLLGIPIHKWASLIWLCGPISGMVQPIVGY 87

QY 74 ASDHWRGRRRPRPIWALSGLILLSLELI PRAGWLAGL-----LCPDPRPLELALLI 126
DB 88 HSDRCTSRFRRRPRPIVAGAGLVTVAVFLI---GYAADIGHSMGQDQPKPKTRAIAPA 144

QY 127 LGVGLLDFCGQVCFPLEALLSDLFR-DPDHCRQAYSVAFMISLGGCLGY-----LL 178
DB 145 LGFWILDVANNTLQGPCRAFLADLSAGNAKKTRTANAFSPFPMAGNVLYGAAGSYRNLY 204

QY 179 PAIDWD-TSALAPYLGTOECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPSL 237
DB 205 KVPFTMTSCDLYCANLKTCCFLSITLL-LIVTFVSLCYVKEKPTPEPTADGKA---- 259

QY 238 SHPCPCRARLAFRNLGALLPRHLQCCRMPTLRFLVAELCSNMALMTFTLFTDFVG 297
DB 260 -----SNVPF--FGEIFGAFKEL-----KRPMMMLLIIVTALNWIAPFLLFDTDMWG 305

QY 298 EGLYQGVPRAPGTEARRHYDEGVRMSGLFLQCAISLVFSLVMDRLVORFGTRAVYLA 357
DB 306 REVYGGNSDATATAASKLYNDGVRAGALGLMNAIVLGFMSLGVWEIGRKLK-GAKRLW 364

QY 358 SVAAPFVAAGATCLSHSVAV-----VTASA---ALTG---FT 388
DB 365 GIVNFIL--AICLAMTVVTVTKQAENHRDHGAKTGPNGVNTAGALTTLFAILGIPQAIT 421

QY 389 FSALQLPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTSFLPGP 435
DB 422 FS-----IPFALASIFSTNSGAGGSLGLVNLAIIVPQMWISVGGGPFDELFGGNIPA- 476

QY 436 KPGAPFNGHVAGGSGLL-----PPPPA 459
DB 477 -----FVLGAIAAASVGLALTVLPSPPDA 502

RESULT 8
S48789
sucrose transport protein - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S48789
R:Buerkle, X.Y.Z.; Frommer, W.B.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48787
A:Accession: S48789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-507 <BUE>
A:Cross-references: UNIPROT:Q40583; UNIPARC:UPI00000A75A6; EMBL:X82276; NID:g575350; PID: submitted to the EMBL Data Library, October 1994
C:Superfamily: common tobacco sucrose transport protein

Query Match 11.1%; Score 317.5; DB 2; Length 507;
Best Local Similarity 24.3%; Pred. No. 2.9e-16;
Matches 125; Conservative 87; Mismatches 203; Indels 99; Gaps 18;

QY 4 RLWRSLLRHRKAQLLVNLTTFGLEVCLAAGITYVPPLLEVGVEEKFTMTVLGIGPV 63
DB 23 KLW-----KIMVASIAAGVQFGWALQSLLTPVQLLGIPIHKFASFWLTCGPIS 72

QY 64 GLVCPVPLLSGSDHWRGRRPRPIWALSGLILLSLELI PRAGWLAGLCCDDP-----R 118
DB 73 GMIVQPVVGYSDNCSSRRFRRRRGFIAGALVTVIAVFLIGFAADL-GHATGDLPGKGSK 131

QY 119 PLEALLIILGVGLLDFCGQVCFPLEALLSDLFRDPDHCRQAYSVAFMISLGGCLGYLL 178

Db 132 PRAIAVGVFWILDVANNMLQGPCRALLADLSGGKARMTSNAFFSFFMAVGNVLGYAA 191
QY 179 PAID-----WDTALAPYLGTQBECLF-GLLTLFLTCVAATLLVAEEAALGTEPA 229
Db 192 GSYRICKIPFPSKTPACDIYCANLKSCEFIAVFLLLSLTILALT--VVRENELPEKDEH 249
QY 230 EGLSAPSLSPHCCPCRLAFRLNGLALLPRLHOLCCRMPTLRLRLFAELCSMMALMTFT 289
Db 250 E-----IDEKAGARSKVPF--FGEIFGALKDL-----PRPMWILLVTLNWIARFPFF 297
QY 290 LFYTDVFGSLGVQVPRAEPGTETARRHYDEGVNMGSLGLFLQCAISLVSFLVMDRLVQRP 349
Db 298 LYDTHMKEVYGG--KVGDG---RLYDLGVHAGALLNLSVWLFMSLSVEFLGKKI 351
QY 350 GTRAVVYLASVAAPFVAAGATCLSHSVAVV-----TASALGTFTFSALQI-- 394
Db 352 G-GVKRLWGLNFVL---AVCMALTVLVTMMAEKSQRYDAHGTLMAPTSGVKIGALTFLA 407
QY 395 -----LPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTS 430
Db 408 VLGIPLAVTFSPFALASIFSSNAGSGQSLGLVNLAIWVQMLVSIAGGPWDDLFGGG 467
QY 431 FLPGPKPGAPFNGHVGAGSG-----LPPPPPA 459
Db 468 NLPG-----FIVGAVAAASGILALTMLPSPPA 495

RESULT 9

S43142
sucrose transport protein - castor bean
N:Alternate names: sucrose carrier
C:Species: Ricinus communis (castor bean)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43142
R:Weig, A.; Komor, E.
A:Description: A sucrose carrier from Ricinus communis.
A:Reference number: S43142
A:Accession: S43142
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-533 <WEI>
A:Cross-references: UNIPROT:Q41152; UNIPARC:UPI00009D016; EMBL:Z31561; NID:G468561; PID
C:Superfamily: common tobacco sucrose transport protein

Query Match 10.9%; Score 311; DB 2; Length 533;
Best Local Similarity 23.3%; Pred. No. 9.5e-16;
Matches 134; Conservative 95; Mismatches 225; Indels 120; Gaps 19;
QY 17 QLLLVNLLTFGLEVCLAAAGITYVPPLLLEVGVBEKFMVTLGIGPVGLVCVPLLSASD 76
Db 37 KVMVASIAGIQFGWALQSLTTPYVQLGIPHTWAAFIWLCGPISGMLVQVIVGHS 96
QY 77 HWRGYRRRPFTWALSGLTLLSLFLIPRA---GWLAG-LLCPDPRPLELALLILGVGL 132
Db 97 RCTSRGRRRPFTASGAFAVIAVFLIGYAADLHLSGDSLDKSPKTRAIAPVGVFWIL 156
QY 133 DFCGQVCTFPLEALLSDLF-RDPDHCROAVSVYAFMISLGGCGYLLPAID-----W 183
Db 157 DVANNMLQGPCRALLADLSGTSOKTRTANALSFVFMVAVGNVLGYAAGAYTHLYKLPFT 216
QY 184 DTSALAPYLGTQBECLFGLTLFLTCVAATLLVAEEAALGTEPAEGL-----SAP 235
Db 217 KTTACDVYCANLKSCEFISIVLLSLTLVLSVYVKEK----PWSPOAVDNAEDDTASQA 272
QY 236 SLSPHCCPCRLAL--AFRNLGALLPRLHOLCCRMPTLRLRLFAELCSMMALMTFTFLYT 293
Db 273 SSSAQMPFPFGEILGAFKNL-----KRPMMILLVTLNWIAPFLLFDT 318
QY 294 DFVGEGLYQGVPAEPGTETARRHYDEGVNMGSLGLFLQCAISLVSFLVMDRLVQREGTRA 353
Db 319 DWMGREVYGG--DSSGSAEQLKLYDRGVAGALGLMLNSVVLGFTSLIGVEVLARGVG-GV 375

QY 354 VYLASVAAPFVAAGATCLSHSVAVVTASALGTFTFSALQILPYTLASLYHREKQVFLPK 413
Db 376 KELWGVNFVL---AVCLAMTV-LVTKQAESt-----RR 405
QY 414 YRGDTGGASSEDLSMTSFLPGPKPGAPFNGHVGAGSGLLPPPPALCASACDVSRVV 473
Db 406 FATVSGGAK-----VP-----LPPP---SGVKAGALALFAV 433
QY 474 VGEPTEARV-VP-----GRGICLDLAILDSAFLLSQAFLSVAFLMGSIVQL--SOS 519
Db 434 MGVPQAITVISIPALASIFSNTSGAGQSLGVNLNLSIVIPQMINVSAAGPMDLPGGN 493
QY 520 VTAYMVVSAAGLGLVAIFYFATQVVFDSKLAKYSA 553
Db 494 LPAFVVGAVALASGIFALTMLPSPQPDMPSAKA 527

RESULT 10

T14339
sucrose-proton transport protein - carrot
N:Alternate names: sucrose/H+ symporter protein
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14339
R:Shakya, R.; Sturm, A.
A:Title: Characterization of source- and sink-specific sucrose/H+ symporters from carrot
A:Reference number: Z17991; MUID:99063785; PMID:9847123
A:Accession: T14339
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-501 <SHA>
A:Cross-references: UNIPROT:O65929; UNIPARC:UPI00000ACFB6; EMBL:Y16766; NID:G2969886; P
A:Experimental source: cultivar Namtaise: leaf
C:Genetics:
C:Gene: SUT1a
C:Superfamily: common tobacco sucrose transport protein

Query Match 10.7%; Score 305.5; DB 2; Length 501;
Best Local Similarity 21.6%; Pred. No. 2.3e-15;
Matches 124; Conservative 91; Mismatches 213; Indels 145; Gaps 14;
QY 18 LLLVNLTLFGLVCLAAAGITYVPPLLLEVGVBEKFMVTLGIGPVGLVCVPLLSASDH 77
Db 30 LLRVASVACGIQFGWALQSLTTPYVQELGIPHANSSIIWLCGPLSGLLVQPIVGHMSDQ 89
QY 78 WRGYRRRPFTWALSGLTLLSLFLIPRAGWAGLL--CPDPRPLELALLILGVGLLDFC 135
Db 90 CTSKYRRRPFTVAGGTAILAVIIIAHSADIGGLIGDITADNKTMAIVAFVIGFWILDVA 149
QY 136 GOVCFPTPEALLSDLF-RDPDHCROAVSVYAFMISLGGCGYLLPAIDWDTSALAPVLT 194
Db 150 NMTGQPCRALLDITGNDARRTRVANAYFSLFMAIGNVLGY-----ATGAYSGW 199
QY 195 OBECLFGLTLFLTC-----VAATLLVAEEAAL-----GPTPEAEG 232
Db 200 YKVFPPSLTSSCTINCANLKSIFYIDIIFIITVISIAKERPRISSODGQFSEDGT 259
QY 233 SAPSLSPHCCPCRLAFRLNGLALLPRLHOLCCRMPTLRLRLFAELCSMMALMTTLFY 292
Db 260 AQ---SGHT-----EEAFLWELFGTFRLLPGSVVIVLLVTLNWIWFFRFILE 305
QY 293 TDFVCEGLYQGVPAEPGTETARRHYDEGVNMGSLGLFLQCAISLVSFLVMDRLVQREGTR 352
Db 306 TDMGREIYGGEP-----NOQGSYSDGVNMGAFGLMNSVVLGITSVLMELCRLWGS 359
QY 353 AVYLASVAAPFVAAGATCLSHSVAVVTASALGTFTFSALQILPYTLASLYHREKQVFLP 412
Db 360 FWM-----GLSNILMTICFFAMLLITFAKNNDY----- 388
QY 413 KYRGDTGGASSEDLSMTSFLPGPKPGAPFNGHVGAGSGGLLPPPPALCASACDVSRVV 472

Db 389 -----GTNPPN---GIVISALIVFA 406
Qy 473 VVGEPTARV-VP-----GRGICLDAILDSAFLLSQVAPSPMGSIQV----- 516
Db 407 ILGILPAAITYSPYALVSTRIESLGLGQGLSMGVNLAIWVQVIVSLSGPMDQLFGGG 466
Qy 517 -SQSVTAYNVSAAGLGLVAIYFATQVVFQKSDL 548
Db 467 NSPAFVVAALSFAAGLIAAIRPRVDKSL 499

RESULT 11
S48788
sucrose transport protein - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S48788
R:Bueckle, X.Y.Z.; Frommer, W.B.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48788
A:Accession: S48788
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <BUE>
A:Cross-references: UNIPROT:Q40167; UNIPARC:UPI00001794EA; EMBL:X82275
C:Superfamily: common tobacco sucrose transporter protein

Query Match 10.4%; Score 297.5; DB 2; Length 428;
Best Local Similarity 25.8%; Pred. No. 7.8e-15;
Matches 114; Conservative 82; Mismatches 163; Indels 83; Gaps 18;
Qy 4 RLWBSLLRHRKAQLLLNLTFTGLEVCLAAAGITYVPPPLLEVGVEEKMTWVLGIPVL 63
Db 25 KLV-----KIIVASIAAGVQFGWALQSLTTPYVQLGIPHRFASFVWLCPGIS 74
Qy 64 GLVCPVLGASDHGRGRPRFPFWALSGLTLLSLFLIPRAGWLAGLLCPDP-----R 118
Db 75 GMTVPVGVYDNCSSRFRGRFPFIAAGALVTIAVFLIGFADLI-GHASGDPGLKSGK 133
Qy 119 PLEALLILGVGLDFCGQVCFPLEALLSDLRDPD-HCRQAYSIVAFMISLGGCLGY- 176
Db 134 PRAIVAVGVFWILDVANNMLQGPCRALLADLSGGKSGKMTANAFSPFKAVGNILGYA 193
Qy 177 -----LLPAIDWD-TSALAPYLGTQECFL-CLLTLLIFLTCVAATLL-----VAEEAALG 224
Db 194 AGSYSLFLKVPFESKTKADMYRANLKSCFFIAIFLLLSLTLLTALTLVRENELPEKEELE 253
Qy 225 PTEPAEGLSAPLSPHCCPCRARLAFRNLGALLPRHLQCCMRPRTLRLFLVAELCSWMA 284
Db 254 IDEKLSGAG-----KSKVFP--FGEIFGALKDL-----PRPMWILLVTCNLWIA 296
Qy 285 LMTFTLFTYDFVGEGLYQGVPRAPGCTEARRHYDEGVRMGSLGFLTQCAISLVFSLVMDR 344
Db 297 WPFPEFLYDTDMAKEVFGG---QVGD--AKLYDLGVAGALGLLQSVVLGFMWSLGVF 350
Qy 345 LVORFGTRAVYLASVAFVPAAGATCLSHSVAVV-----TASAAATGFT----- 388
Db 351 LGKKIG-GAKRLWGLNFVL---AICLAMTILTVKMAEKSRRGHDAAGTLMGTPPGVKIGA 406
Qy 389 ---FSALQI-----LPYTLA 400
Db 407 LLLFAALGICPLAVTFSIPFALA 428

RESULT 12
S38657
sucrose transport protein ptpl - common plantain
N:Alternate names: sucrose transporter ptpl
C:Species: Plantago major (common plantain)
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S38657
R:Gahrtz, M.; Stolz, J.; Sauer, N.
submitted to the EMBL Data Library, November 1993

A:Reference number: S38657
A:Accession: S38657
A:Molecule type: mRNA
A:Residues: 1-510 <GAH>
C:Cross-references: UNIPROT:Q40938; UNIPARC:UPI00000A55AF; EMBL:X75764; NID:G415987; PI1
C:Genetics:
A:Gene: ptpl
C:Superfamily: common tobacco sucrose transporter protein
C:Keywords: sugar transport

Query Match 10.3%; Score 294; DB 2; Length 510;
Best Local Similarity 24.7%; Pred. No. 1.7e-14;
Matches 126; Conservative 77; Mismatches 199; Indels 108; Gaps 19;
Qy 18 LLLVNLTLFTGLEVCLAAAGITYVPPPLLEVGVEEKMTWVLGIPVLGVCVPLLGASDPH 77
Db 29 IFLVAAIAAGVQFGWALQSLTTPYVQLGIPHRKASVYIWLCPGISGMIVQVPVGFSDN 88
Qy 78 WRGRYRRRPFITWALSGLIL-LSLFLIPRAGWLAGL-----LCPDRPRLLEALLILGV 129
Db 89 CTSRFRGRFPFI-AGAGLVGVAVVLI---GFAADLGHAGDSGLDGLKFPRAIGVVFVGF 144
Qy 130 GLLDFCGQVCFPLEALLSDLF-RDPDHCQRQAYSIVAFMISLGGCLGYLLPAID----- 182
Db 145 WILDVANMLQGPCRALLADLSGGNTKKMANANSPFSPFMAVGNVLGYAAGSYSRMYKV 204
Qy 183 --WDTSAAPYLGTQEEC-LFGLLTLLIFLTCVAATLL-----VAEEAALGPTPEAELSA 234
Db 205 PFSKTKACDIYCANUKSCFIISITLITLITLUALSIVREKRVABEQV---TAACKGFKI 261
Qy 235 PSLSPHCCPCRARLAFRNLGALLPRHLQCCMRPRTLRLFLVAELCSMMALMTFTLYFD 294
Db 262 P-----VFPELFGALKDLPRPMWVLLVLTALNWIAMWFGFLFDTD 301
Qy 295 FVGEGLYQGVPRAPGCTEARRHYDEGVRMGSLGFLTQCAISLVFSLVMDRLVQREG---- 350
Db 302 MWGREVY-GETQCHKAPELAVIYNGVSAGALGLMLNSIVLGFASLGVOYMARALGVKVR 360
Qy 351 -----TFANVLA-SVAAPVAAAGATCLSHSVAVVTASAALTG--FTFSALQI----- 394
Db 361 LMGVNFIALICLMTIVITVKASHRYPYNSGVLOTPTSSVKIGALVFSALGIPLAITF 420
Qy 395 -LPYTLASLYHREKQVFLPKYRGDTGGASSEDLSL-----MTSFLPGPKRG---- 438
Db 421 SVFPFALASIV-----STTTGSGQGLSLGVNLAIVIPQMIIVSVASGPMWDMAFG 468
Qy 439 ----APFPNGHVAGGSG-----LLPPPPA 459
Db 469 GGNLPFVVGAVAAAAAGSIFAFMTLPSPPPA 498

RESULT 13
S51114
sucrose-proton symporter - beet
C:Species: Beta vulgaris (beet)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51114
R:Westram, A.; Eckhardt, U.; Frommer, W.B.; Riesmeier, J.W.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence of a sugar beet sucrose transporter cDNA.
A:Reference number: S51114
A:Accession: S51114
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-523 <WES>
A:Cross-references: UNIPROT:Q39438; UNIPARC:UPI00000A55B7; EMBL:X83850; NID:G633171; PI1
C:Superfamily: common tobacco sucrose transporter protein

Query Match 10.3%; Score 294; DB 2; Length 523;
Best Local Similarity 24.3%; Pred. No. 1.8e-14;
Matches 125; Conservative 78; Mismatches 199; Indels 112; Gaps 20;
Qy 17 QLLVNLTLFTGLEVCLAAAGITYVPPPLLEVGVEEKMTWVLGIPVLGVCVPLLGASD 76

Db 38 KLAIVASIAAGVQFGWALQSLTTPYVQLLGIPTWAPYIWLCPISGMIVQPTGVYSD 97
 QY 77 HWRGRYRRPFTWALSGLTLLSLFLPRAGMLA--GLLCPD-----PRLELALLIGV 129
 Db 98 RCTSKGRRRPFTI---AVGATLVGFVSLVGLFRAADIGHATGDPNGNVKPRATIAFVVGF 154
 QY 130 GLLDFCGQVFTFLEALLSLDFRDPD--HCRQAYSVYAFMISLGGCLGY-----LLP 179
 Db 155 WILDVANNTLQGPCRALLADMAAGSQAKRYANAFSFFMALNIGGAGSYGRLYTVFP 214
 QY 180 AIDWDTSAAPYLGTOBECLFGLTLLFTCVAAATLLVAEEAALGPTPEAGLSAPSLSP 239
 Db 215 FT--HTKACDTCYCANLKSCFFITLLVLTILALSVRER----PFTLEIOEEENLKN 268
 QY 240 HCCPCRLARLAFNLGALLPRLHOLCCRMPTLRLFLVAELCSNMALMTFTFLYDFVGE 299
 Db 269 NTGGC--ARLPF--FGQLFGALKDL-----PKMILLVLTCLNWIAPFLLFDTDMWKE 321
 QY 300 LYQGVPAEPTGEARRHYDEGVRMSGLGLFLOCAISLVFSLVMDRLVQRF--TRAVYLA 357
 Db 322 VYGGT-----VGEGRAYDMGVHAGALGLMINSVLGIMSLGIEKLARLVGGYKRLWGV 375
 QY 358 SVAAPFVAAGATCLSHSAVVVTA-----ALTF 387
 Db 376 NLIL-----AVCLAMTI-LVTKSAEHYRATHVPGAIGPPLPPGVKGALAIFAVLGI 428
 QY 388 TFSALQILPYTLASLYHREK-----QVFLPKYRGDTGASSEDLSMT 429
 Db 429 PLAITSIPALASIFSASSGSGGLSLGVNLAIIVPQMVFVSTGPM-----DAL-- 480
 QY 430 SFLPGPKGAPFPNGHVAGGSG-----LLPPPP 458
 Db 481 -FGGNLPA--FVGVAAATASAILSTLLPPPP 511

RESULT 14

F96741
 probable sucrose transport protein F17M19.4 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F96741
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96741
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-512 <STO>
 A:Cross-references: UNIPROT:Q9C8X2; UNIPARC:UPI0000048458; GB:AE005173; NID:g6978914; P1
 C:Genetics:
 A:Map position: 1
 C:Superfamily: common tobacco sucrose transport protein

Query Match 10.2%; Score 292.5; DB 2; Length 512;
 Best Local Similarity 23.8%; Pred. No. 2.2e-14;
 Matches 120; Conservative 87; Mismatches 211; Indels 87; Gaps 18;

QY 17 QLLLVNLLTFGLVECLAAGITYVPPLLLEVGVEEKFMTVMVLGIPVLGVCVPLLSASD 76
 Db 33 KIISVASIAAGVQFGWALQSLTTPYIQLLGIPTWAPYIWLCPISGMIVQPTGVYSD 92
 QY 77 HWRGRYRRPFTWALSGLTLLSLFLPRAGMLA-----LCPDPRLELALLIGV 129

Db 93 RCESEFRGRRPFTIAGVALVAVSVFLI---GFAADMGHSFGDKLENKVRTRAIIFLTGTF 149
 QY 130 GLLDFCGQVFTFLEALLSLDFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL 178
 Db 150 WFLDVANNTLQGPCRAFLADLAAGDAKTRVANACFSFFMAVGNVLYGAAGSYTNLHKMF 209
 QY 179 PAIDWDTSAAPYLGTOBECLFGLTLLFTCVAAATLLVAEEAALGPTPEAGLSAPSL 238
 Db 210 PFT--MTKACDIYCANLKCTFFLSITLLIVTFSSLSLWYVKDK----QWSPQDGKEBKS 263
 QY 239 PHCCPCRLARLAFNLGALLPRLHOLCCRMPTLRLFLVAELCSNMALMTFTFLYDFVGE 298
 Db 264 -----SLFF--FGEIFGAVR-----HMKRPMVMLLIVTINWIAFFPILYDITDMGR 309
 QY 299 GLYQGVPAEPTGEARRHYDEGVRMSGLGLFLOCAISLVFSLVMDRLVQRFGRVAVVLAS 358
 Db 310 EYVGG--NSDGDERSKLYDQGVQAGALGLMENSILLFPVSLGVESIGRKG--GAKELWG 366
 QY 359 VAAFPVAAGATCLSHSAVVVTA-----SAALTGTFTFSALQIL----- 395
 Db 367 CVNFILAI--LMTVLVTKSAEHRETAGPLAGPSSGIGKAGVSLFTVLGIPLAITYS 423
 QY 396 -PYTLASLYHREKQVFLPKYRGDTGASSEDLSMTSFLPGKP-----GAPFPN---GHVG 447
 Db 424 IPFALASIFSTNSGAGCGGLSLGVNLTAICIPQMIVFSSGPLDAQFGGGLPSPFVVGAI 483
 QY 448 AGSGGL-----PPP--PALCGA 463
 Db 484 AAVSGVIALTVLPSPPDAPAMSGA 508

RESULT 15

T02982
 probable sucrose transport protein - rice
 C:Species: Oryza sativa (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02982
 R:Hirose, T.; Imaiizumi, N.; Scofield, G.N.; Furbank, R.T.; Ohsugi, R.
 Plant Cell Physiol. 38, 1389-1396, 1997
 A:Title: cDNA cloning and tissue specific expression of a gene for sucrose transporter
 A:Reference number: Z14809; MUID:98182940; PMID:9522469
 A:Accession: T02982
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-537 <HIR>
 A:Cross-references: UNIPROT:O49838; UNIPARC:UPI00000A2688; EMBL:D87819; NID:g2723470; P
 A:Experimental source: cultivar Nipponbare, leaf
 C:Genetics:
 A:Gene: SUT1
 C:Superfamily: common tobacco sucrose transport protein

Query Match 10.2%; Score 292; DB 2; Length 537;
 Best Local Similarity 26.7%; Pred. No. 2.6e-14;
 Matches 115; Conservative 72; Mismatches 167; Indels 76; Gaps 19;

QY 17 QLLLVNLLTFGLVECLAAGITYVPPLLLEVGVEEKFMTVMVLGIPVLGVCVPLLSASD 76
 Db 51 RUIISGMVAGVQVYQWALQSLTTPYVQTLGLSHALTSPMWLCGPIAGWVQVPCVGLYSD 110
 QY 77 HWRGRYRRPFTWALSGLTLLSLFLI---PRAGWLAGLLCPD-----PRPLELALLIL 127
 Db 111 RCTSKWRRRPVILTGCVLICLAVVVGFSADIGYAMGDTKEDCSYVHSGRMAAIVVYL 170
 QY 128 GVLGLDFCCQVCFPTLEALLSLDF--RDPDHCRQAYSVYAFMISLGGCLGYLLPAID--- 182
 Db 171 GFWLLDFSNNTVOGPARALMADLSGRHFGP---TANSIFCSNMWMLNIGYSSGSTNNWH 227
 QY 183 -WDTSAAPYLGTOBEK-----LFG--LLTLIFLT--CVAATLIVABE-----AALGPT- 226
 Db 228 KW-----FPFLKTRACCEACANLKGAFLVAVFLSLCLVLTILIFAKEVFPKGNAL--PTK 281
 QY 227 --EPAEGLSAPLSHCCPCRLARLAFNLGALLPRLHOLCCRMPTLRLFLVAELCSNWA 284

Db 282 SNEPAEPECTG-----PLAVLKGFRNLPTGMPV-----LIVTGL-TWLS 320
QY 285 LMTFTLFYTDVFVGEGLYQGVPR-AEPGTEARRHYDEGVRMGSLGLFLOCAISLVFSLYMD 343
Db 321 WFFFLYDIDWNGREIYHDPKGTDPQIEA---FNOGVPRAGAGLLNSIVLGFSSFLIE 377
QY 344 RLVRFGTTRAVYLASVAAPFVAAGATCL-----SHSVA--VVTASAAALTGFTFSALQ 393
Db 378 PMCRKVGPVRVWVTSNFLVCIAAATALI SFWSLKDHFHGTGVTOKAITADKSIKAVCLVLFA 437
QY 394 ILPYTLASLY 403
Db 438 FLGVPLAVLY 447

Search completed: May 27, 2006, 04:05:32
Job time : 45 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 03:56:28 ; Search time 302 Seconds
(without alignments)
1693.820 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 2861

Sequence: 1 MVQRLWVSRLRRHRAQLLL.....AIYFATQVVFDKSLAKYSA 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2861	100.0	553	1 S45A3_HUMAN	Q96Jt2 homo sapien
2	2798	97.8	553	1 S45A3_MACFA	Q95K15 macaca fasc
3	2602	90.9	553	1 S45A3_MOUSE	Q8k0h7 mus musculu
4	1375	48.1	578	2 Q4SKEL_TETNG	Q4skel tetraodon n
5	1366	47.7	550	2 Q6PCJ0_XENLA	Q6pcj0 xenopus lae
6	1291	45.1	560	2 Q6PCJ0_XENLA	Q6pcj0 xenopus lae
7	1156	40.4	231	2 Q658X7_HUMAN	Q658x7 homo sapien
8	621	21.7	555	2 Q7Q8T1_ANOGA	Q7q8t1 anopheles g
9	567.5	19.8	618	2 Q6NL41_DROME	Q6nl41 drosophila
10	519.5	18.2	599	2 Q9VSV1_DROME	Q9vsv1 drosophila
11	491	17.2	675	2 Q4R136_TETNG	Q4r136 tetraodon n
12	489.5	17.1	530	1 S45A2_MOUSE	P58J55 mus musculu
13	489.5	17.1	530	2 Q541S3_MOUSE	Q541s3 mus musculu
14	488.5	17.1	530	1 S45A2_HUMAN	Q9unx9 homo sapien
15	488.5	17.1	614	2 Q7Q8Q4_ANOGA	Q7q8q4 anopheles g
16	487	17.0	569	2 Q4SOA7_TETNG	Q4soa7 tetraodon n
17	486.5	17.0	532	2 Q4L888_PIG	Q4l888 sus scrofa
18	484.5	16.9	530	2 Q8C204_MOUSE	Q8c204 mus musculu
19	477.5	16.7	548	2 Q566F3_XENLA	Q566f3 xenopus lae
20	471	16.5	549	2 Q5M7S3_XENTR	Q5m7s3 xenopus tro
21	469.5	16.4	460	2 Q6P2P0_HUMAN	Q6p2p0 homo sapien
22	466	16.3	804	2 Q4RX49_TETNG	Q4rx49 tetraodon n
23	457.5	16.0	782	1 S45A1_HUMAN	Q9y2w3 homo sapien
24	456	15.9	576	2 Q90274_ORYLA	Q90274 oryzias lat
25	455	15.9	751	2 Q566E3_RAT	Q566e3 rattus norv
26	451	15.8	751	1 S45A1_MOUSE	Q8bi7 mus musculu
27	449.5	15.7	529	2 Q2PUG5_CANFA	Q2pug5 canis famil
28	446	15.6	751	1 S45A1_RAT	Q8k4s3 rattus norv
29	436	15.2	785	2 Q3V0B8_MOUSE	Q3v0b8 mus musculu
30	434	15.2	521	2 Q7Q8Q7_ANOGA	Q7q8q7 anopheles g
31	431	15.1	425	2 Q7Q8Q6_ANOGA	Q7q8q6 anopheles g

32	415	14.5	740	2 Q5BKX6_HUMAN	Q5bkx6 homo sapien
33	415	14.5	798	2 Q6ZRI2_HUMAN	Q6zri2 homo sapien
34	396.5	13.9	429	2 Q5TLW0_9CICH	Q5tlw0 neolamprolo
35	396	13.8	720	2 Q6PDG3_MOUSE	Q6pdg3 mus musculu
36	394.5	13.8	754	2 Q7KWK4_DICDI	Q7kwk4 dictyosteli
37	391.5	13.7	429	2 Q5TLW1_9CICH	Q5tlw1 lamprologus
38	391.5	13.7	429	2 Q5TLW4_ALTCL	Q5tlw4 altolamprol
39	390.5	13.6	429	2 Q5TLW2_9CICH	Q5tlw2 astatotilap
40	387.5	13.5	429	2 Q5TLW3_9CICH	Q5tlw3 aulonocara
41	378	13.2	460	2 Q7Q8Q5_ANOGA	Q7q8q5 anopheles g
42	369.5	12.9	2176	2 Q4SJ20_TETNG	Q4sj20 tetraodon n
43	347.5	12.1	515	2 Q6S803_DAUCA	Q6s803 daucus caro
44	347.5	12.1	515	2 Q9FNR6_DAUCA	Q9fnr6 daucus caro
45	346.5	12.1	501	2 Q9SQK6_VITVI	Q9sqk6 vitis vinif

ALIGNMENTS

RESULT 1
S45A3_HUMAN
ID S45A3_HUMAN STANDARD; PRT; 553 AA.
AC Q96JT2;
DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Solute carrier family 45 member 3 (Prostate cancer-associated protein
DE 6) (Protein).
DE Name=SUC45A3; Synonyms=PCANAP6, PRST;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=Prostate;
RX MEDLINE=21139094; PubMed=11245466;
RA Xu J., Kalos M., Stolk J.A., Zasloff E.J., Zhang X., Houghton R.L.,
RA Filho A.M., Nolasco M., Badaro R., Reed S.G.;
RA "Identification and characterization of prostein, a novel prostate-
specific protein.";
RA Cancer Res. 61:1563-1568 (2001).
RL [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=PNS;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Roshylyuk S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP TISSUE SPECIFICITY.
RX PubMed=14957204; DOI=10.1038/sj.bjc.6601642;
RA Kieselring A., Stevanovic S., Fuessel S., Weigle B., Rieger M.A.,
RA Temme A., Rieber E.P., Schmitz W.;
RT "Identification of an HLA-A(*)0201-restricted T-cell epitope derived

RT from the prostate cancer-associated protein prostein.";
RL Br. J. Cancer 90:1034-1040(2004).
CC -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -|- TISSUE SPECIFICITY: Prostate-specific. Expressed in all prostatic
CC glandular cells. Expressed both in normal and cancerous prostates.
CC -|- INDUCTION: Up-regulated by androgens.
CC -|- MISCELLANEOUS: Marker for prostate cells. May be used, in case of
CC prostate cancers, as a target antigen for prostate carcinomas-
CC directed cytotoxic T-cell lymphocytes.
CC -|- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AY033593; AAK54386.1; -; mRNA.
DR EMBL: BC050416; AAH50416.1; -; mRNA.
DR Ensembl: ENSG00000158715; Homo sapiens.
DR HGNC: HGNC:8642; SLC45A3.
DR MIM: 605097; Gene.
DR MIM: 608319; Gene.
DR InterPro: IPR011701; MFS_1.
DR Pfam: PF07690; MFS_1; 1.
DR Membrane; Transmembrane; Transport.
KW CHAIN 1 553 Solute carrier family 45 member 3.
FT FT TRANSMEM 19 39 /FtId=PRO_0000122519.
FT FT TRANSMEM 52 72 1 (Potential).
FT FT TRANSMEM 88 108 2 (Potential).
FT FT TRANSMEM 120 140 3 (Potential).
FT FT TRANSMEM 161 181 4 (Potential).
FT FT TRANSMEM 198 218 5 (Potential).
FT FT TRANSMEM 275 295 6 (Potential).
FT FT TRANSMEM 323 343 7 (Potential).
FT FT TRANSMEM 353 373 8 (Potential).
FT FT TRANSMEM 382 402 9 (Potential).
FT FT TRANSMEM 522 542 10 (Potential).
FT FT COMPTAS 455 458 Poly-Pro.
SQ SEQUENCE 553 AA; 59323 MW; 0AFA23FBC742A667 CRC64;

Query Match 100.0%; Score 2861; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.7e-210; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0;

QY 1 MVQRLWVSRLLRHRKAQLLLVNLTLTFLGVLCLAAAGITVVPPLLEVGVEEKFMTWVLGIG 60
DB 1 MVQRLWVSRLLRHRKAQLLLVNLTLTFLGVLCLAAAGITVVPPLLEVGVEEKFMTWVLGIG 60

QY 61 PVLGLVCPVLLGSDHWRGRRRPFIAWLSGILLSLFLIPRAGWLAGLLCPDRPL 120
DB 61 PVLGLVCPVLLGSDHWRGRRRPFIAWLSGILLSLFLIPRAGWLAGLLCPDRPL 120

QY 121 ELALLILGVLDFCGQVCFPLEALLSDLPDCHCRQAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVLDFCGQVCFPLEALLSDLPDCHCRQAYSVYAFMISLGGCLGYLLPA 180

QY 181 IDWDTLSALAPYLGTOECLFGLLTILFTCVAAATLLVAEEALGTEPAEGLSAPLSPH 240
DB 181 IDWDTLSALAPYLGTOECLFGLLTILFTCVAAATLLVAEEALGTEPAEGLSAPLSPH 240

QY 241 CCPCARLARAFNLGALLPRHLQCCRMPTLRLLFVAELCSWMAWMTFTLYTFDVGEG 300
DB 241 CCPCARLARAFNLGALLPRHLQCCRMPTLRLLFVAELCSWMAWMTFTLYTFDVGEG 300

QY 301 YQGVPAEPTGTEARRHYDEGVGMGSLGLFLQCAISLVFSLVMDRLVQRFGRVAVLASVA 360
DB 301 YQGVPAEPTGTEARRHYDEGVGMGSLGLFLQCAISLVFSLVMDRLVQRFGRVAVLASVA 360

QY 361 AFPVAAGATCLSHSVAVVTASALTGFTESALQILPYTLASLYHREKOVFLPKYRGDTGG 420
DB 361 AFPVAAGATCLSHSVAVVTASALTGFTESALQILPYTLASLYHREKOVFLPKYRGDTGG 420

QY 421 ASSSDSLMTSFLPGPKGAPFPNGHVAGSGGLPPBALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSSDSLMTSFLPGPKGAPFPNGHVAGSGGLPPBALCGASACDVSVRVVVGEPTEA 480

QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYPATQ 540
DB 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYPATQ 540

QY 541 VVFDKSLAKYSA 553
DB 541 VVFDKSLAKYSA 553

RESULT 2
S45A3 MACFA STANDARD; PRT; 553 AA.
ID S45A3 MACFA
AC Q95K15; Q95K05;
DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Solute carrier family 45 member 3 (Prostate cancer-associated protein
DE 6) (Protein).
GN Name=SLC45A3; Synonyms=PCANAP6, PRST; ORFNames=QmOA-10594, QmOA-11310;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OC NCBI_taxid=9541;
OX [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Medulla oblongata, and Temporal cortex;
RC Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -|- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AB060851; BAB46871.1; -; mRNA.
DR EMBL: AB062977; BAB60745.1; ALT_INIT; mRNA.
DR InterPro: IPR011701; MFS_1.
DR Pfam: PF07690; MFS_1; 1.
KW Membrane; Transmembrane; Transport.
KW CHAIN 1 553 Solute carrier family 45 member 3.
FT FT TRANSMEM 19 39 /FtId=PRO_0000122520.
FT FT TRANSMEM 52 72 1 (Potential).
FT FT TRANSMEM 88 108 2 (Potential).
FT FT TRANSMEM 120 140 3 (Potential).
FT FT TRANSMEM 161 181 4 (Potential).
FT FT TRANSMEM 198 218 5 (Potential).
FT FT TRANSMEM 275 295 6 (Potential).
FT FT TRANSMEM 323 343 7 (Potential).
FT FT TRANSMEM 353 373 8 (Potential).
FT FT TRANSMEM 382 402 9 (Potential).
FT FT TRANSMEM 522 542 10 (Potential).
FT FT COMPTAS 455 458 Poly-Pro.
FT FT COMPTAS 165 165 A -> T (in Ref. 1; BAB60745).
FT FT CONFLICT 342 342 M -> V (in Ref. 1; BAB60745).
FT FT CONFLICT 342 342 M -> V (in Ref. 1; BAB60745).
SQ SEQUENCE 553 AA; 59393 MW; 0718F3A91FB3F1E CRC64;

Query Match 97.8%; Score 2798; DB 1; Length 553;
Best Local Similarity 98.2%; Pred. No. 1.2e-205;
Matches 542; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHRKAQLLLVNLTLTFLGVLCLAAAGITVVPPLLEVGVEEKFMTWVLGIG 60

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Db 1 MVQRLVSVRLRRKRAQALLINLLTFGLVCLAAAGITYVPPPLLVLEGVBEKFWMTVLGIG 60
QY 61 PVGLGVCVPLGSGASDHWRGVRGRRPFTWALSGLTLLSLFLTPRAGWLAGLLCPDPRPL 120
Db 61 PVGLGVCVPLGSGASDHWRGVRGRRPFTWALSGLTLLSLFLTPRAGWLAGLLCPDPRPL 120
QY 121 ELALLIGVGLDFCQGVCFPTPLLEALLSLDFRDPDRCRQAYSAYAFMISLGGCGLYLLPA 180
Db 121 ELALLIGVGLDFCQGVCFPTPLLEALLSLDFRDPDRCRQAYSAYAFMISLGGCGLYLLPA 180
QY 181 IDWDTSAALPYLGTQCECLFGLLTFLFCVAATLVAAEALGPTPEAGLSAPLSLPH 240
Db 181 IDWDTSAALPYLGTQCECLFGLLTFLFCVAATLVAAEALGPTPEAGLSAPLSLPH 240
QY 241 CPCPCARLARFRNLGALLPRHLQCCMRPTLRRLFVAELCSWMLMTFTFLFYTFDFVGEGL 300
Db 241 CPCPCARLARFRNLGALLPRHLQCCMRPTLRRLFVAELCSWMLMTFTFLFYTFDFVGEGL 300
QY 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVORFGTRAVYLASVA 360
Db 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVORFGTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGPEPTA 480
Db 421 TSSEDSLMTSFLPGPKPGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGPEPTA 480
QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYS 552
Db 541 VVFDKSDLAKYS 552

RESULT 3
*ID S45A3_MOUSE STANDARD; PRT; 553 AA.
AC O9K0H7; Q8K252; Q8R110;
DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Solute carrier family 45 member 3 (Prostate cancer-associated protein
DE 6) (Protein).
GN Names=Slc45a3; Synonyms=Pcanap6, Prst;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=C57BL/6J; TISSUE=Urinary bladder.
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Altshuler D., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
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RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
RA Tamoja K., Tan S.-L., Tang S., Taylor R., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimmiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RN Science 309:1559-1563 (2005).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon, Liver, and Mammary tumor.
RX MEDLINE=2238257; PubMed=12477912; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Skalska U., Smalish D.E.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RP TISSUE SPECIFICITY.
RX PubMed=14561649; DOI=10.1095/biolreprod.103.021493;
RA Hsia N., Cornwall G.A.;
RT "DNA microarray analysis of region-specific gene expression in the
RT mouse epididymis.";
RC Biol. Reprod. 70:448-457 (2004).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in the epididymis.
CC -!- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
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CC EMBL; AK035428; BAC29063.1; -; mRNA.
CC EMBL; BC024519; AAH24519.1; -; mRNA.
CC EMBL; BC031381; AAH31381.1; -; mRNA.
CC EMBL; BC034084; AAH34084.1; -; mRNA.
CC Ensembl; ENSMUSG0000026435; Mus musculus.
CC MGI; MGI:1922082; Slc45a3.
CC GO; GO:0016021; C-integral to membrane; TAS.
CC InterPro; IPR011701; MFS_1.
CC Pfam; PF07690; MFS_1.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 NUCLEOTIDE SEQUENCE.
 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 ADAMC.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards J., Ashburner M., Henderson S.N.,
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 Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke A., Davenport L.B., Davies P.,
 de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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 Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 Liu X., Mattet B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kimons I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong X., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*."
 Science 287:2185-2195 (2000).
 [2]
 NUCLEOTIDE SEQUENCE.
 MEDLINE=22426065; PubMed=12537568;
 Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 melanogaster

QY 453 LPPPPALCGASACDVSRVVVVGTEPTEARVVP---GRGICLDLAIDLDSAFLLSQVAPSLF 509
Db 533 -----EIVPLKQARGLCTDVAIISSMVFIAQLIVSL 564
QY 510 MGSIVQLSQSVTAYMVAAGLGLVAIYATQVVF 543
Db 565 VGPLVSMWDTTCALVYASTFLSLAATAAMFVLY 598
RESULT 11
Q4R136_TETNG
ID Q4R136_TETNG PRELIMINARY; PRT; 675 AA.
AC Q4R136;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 8 SCAP15044, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG0034054001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasiiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Scher E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CAA01015044; CAG11946.1; -; Genomic_DNA.
DR NON_TER 675
SQ SEQUENCE 675 AA; 435DF19P4D3533B CRC64;
Query Match 17.2%; Score 491; DB 2; Length 675;
Best Local Similarity 24.4%; Pred. No. 8.2e-29;
Matches 165; Conservative 79; Mismatches 199; Indels 232; Gaps 17;
QY 26 FGLEVCLAAGITVVPPLLVGVGVEEKFMVTMLVGLVGPVPLVGLSADHWGRYGR 85
Db 63 FGREFCYMETALVTPVLLQIGLPEQYSLTWFLSPILGLVFTFVIGTASDRCVLWGR 122
QY 86 RPFIALSGLIL--SLFLIPRAGWLAGLLC---PDRPLELALLGVGLLDFCQGVCF 140
Db 123 RPFIALCGALLGVALFL---NGSLIGLSVGRPGSQPIGLVLTGLVGVVLDPSADAAE 179
QY 141 TPEALLSDFRPDPHCRQAYSVAFMISLGGCLGYLLPAIDWDTSALAPYLGTQECLEF 200
Db 180 GPIRAYLLDV-ADTERQDMALNTHAFSAGLGGVAGVMGLGLDWTGTALGRAFKSQGVLF 238

QY 201 GLTLTFLITCV-----AATLL--VAEE- 220
Db 239 LPASIIIFIISVILHLSIPEQPPVTSQKAAESSGSSQTSFRAISQALPLDLAAEED 298
QY 221 --AAL-----GPT-----EPAGLSAPLSPHC----- 241
Db 299 FSAAQQNDCELNGPTNLQPPDPVGHQOQTKAVNGASPGASSGHCAVKGQOTSTRFT 358
QY 242 -----CPCRL-----AFRLGA 255
Db 359 NHPSSTSASPRPHPTFFRQPSFTFSYGRVGRQFRRLRTAPSRPOPITTSRLNDLSE 418
QY 256 LPLRLHQ-----LCCRMPTLRLRFLVAELCSMMALMT 287
Db 419 LPQRLDRQLQLSTLSSEGSNNLLTKCLLFLSSQMPKQLWRCLCHLLTWFPSIMA 478
QY 288 FTLYFTDFVGEGLYQGVPRAPRPGTEARRHYDEGRVMSGLGLFLOCAISLVSLVMDRLVQ 347
Db 479 EAVFYTFDFMGQVIYHGDPTAPANSTDLQNYNRGVQMGCLVVVYATAAAYCSAILQKYLD 538
QY 348 RF--GTRAVVLAASVAAPPAAGATCLSHSVAVVTASAALTGFTFSALOILPYTLASLYHR 405
Db 539 NFDLSIKIYIVTGLTGFSGAGTAFIAFPNVVYVAMWISSMGVISMISYCPYALLGOYHE 598
QY 406 EKQVFLPKYRGDTGCGASSEDLSMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASA 465
Db 599 IKEV-----C 603
QY 466 CDVSVRVVVGTEPTEARVVRGICLDLAIDLDSAFLLSQVAPSLFMSGISVOLSOVATYMW 525
Db 604 SDTSI-----PANTR-----RGFIDCAILSCQVYSQILVASALGSDVAVGSRVIPA 653
QY 526 SAAG---LGLVAIYF 537
Db 654 VASGGSFLGLTACF 668
RESULT 12
S45A2_MOUSE
ID S45A2_MOUSE STANDARD; PRT; 530 AA.
AC P58355;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 16-NOV-2001, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Membrane-associated transporter protein (AIM-1 protein) (Melanoma
DE antigen AIM1) (Solute carrier family 45 member 2) (Underwhite
DE protein).
GN Name=SLC45A2; Synonyms=Aim1, Matp, uw;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=ddy; TISSUE=Eye, Kidney, and Uterus;
RX MEDLINE=21372467; PubMed=11479596; DOI=10.1038/ng584;
RA Fukunachi S., Shimada A., Shima A.;
RT "Mutations in the gene encoding B, a novel transporter protein, reduce
RT melanin content in medaka."
RL Nat. Genet. 28:381-385 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANTS UW-DBR ASN-153 AND PRO-435.
RX MEDLINE=21473748; PubMed=11574907;
RA Newton J.M., Cohen-Barak O., Hagiwara N., Gardner J.M., Davison M.T.,
RA King R.A., Brilliant M.H.;
RT "Mutations in the human orthologue of the mouse underwhite gene (uw)
RT underlie a new form of oculocutaneous albinism, OCA4."
RL Am. J. Hum. Genet. 69:981-988 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX PubMed=16141072; DOI=10.1126/science.1112014;

RX PubMed=14722913; DOI=10.1002/humu.10311;
RA Runderhagen U., Zuehlke C., Oritz S., Schwinger E.,
RA Kaemann-Kellner B.;
RT "Mutations in the MATP gene in five German patients affected by
RT oculocutaneous albinism type 4.";
RL Hum. Mutat. 23:106-110(2004).
RN [7]
RP VARIANTS LYS-272; LEU-374 AND LEU-507.
RX PubMed=1545243; DOI=10.1007/s00414-004-0490-z;
RA Yuasa I., Umetsu K., Watanabe G., Nakamura H., Endoh M., Irizawa Y.;
RT "MATP polymorphisms in Germans and Japanese: the L374F mutation as a
RT population marker for Caucasoids";
RL Int. J. Legal Med. 118:364-366(2004).
RN [8]
RP VARIANT OCA4 ASN-157.
RX PubMed=15656822; DOI=10.1111/j.1365-2133.2005.06403.x;
RA Suzuki T., Inagaki K., Fukui K., Obana A., Lee S.-T., Tomita Y.;
RT "A Korean case of oculocutaneous albinism type IV caused by a D157N
RT mutation in the MATP gene.";
RL Br. J. Dermatol. 152:174-175(2005).
CC -!- FUNCTION: Melanocyte differentiation antigen. May transport
CC substances required for melanin biosynthesis (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein; melanosome (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=AIM-1a;
CC IsoId=Q9UMX9-1; Sequence=Displayed;
CC Name=AIM-1b;
CC IsoId=Q9UMX9-2; Sequence=VSP_006297, VSP_006298, VSP_006299;
CC Name=AIM-1c;
CC IsoId=Q9UMX9-3; Sequence=VSP_006296;
CC -!- TISSUE SPECIFICITY: Expressed in most melanoma cell lines and
CC melanocytes.
CC -!- DISEASE: Defects in SLC45A2 are the cause of oculocutaneous
CC albinism type 4 (OCA4) [MIM:606574]. OCA4 is an autosomal
CC recessive disorder of pigmentation characterized by reduced
CC biosynthesis of melanin in the skin, hair and eyes. It leads to
CC reduced visual acuity.
CC -!- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 188.
CC -!- CAUTION: The described alternatively spliced isoforms are inferred
CC using information from ESTs.
CC -!- DATABASE: NAME=Mutations of the MATP gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/matpmt.htm".
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF172849; AAD51812.1; -; mRNA.
DR EMBL: BC003597; AA03597.1; ALT_FRAME; mRNA.
DR GenBank: U000000164175; Homo sapiens.
DR HGNC: HGNC:16472; SLC45A2.
DR MIM: 606574; gene.
DR MIM: 606574; phenotype.
KW Albinism; Alternative splicing; Antigen; Disease mutation;
KW Glycoprotein; Melanin biosynthesis; Membrane; Polymorphism;
KW Sensory transduction; Transmembrane; Vision.
KW CHAIN 1 530 Membrane-associated transporter protein.
FT FTId=PRO_0000122517.
FT TOPO_DOM 1 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 1 (potential).
FT TOPO_DOM 68 68 Extracellular (Potential).
FT TRANSMEM 69 89 2 (potential).
FT TOPO_DOM 90 110 Cytoplasmic (Potential).
FT TRANSMEM 111 131 3 (potential).
FT TOPO_DOM 132 138 Extracellular (Potential).
FT TRANSMEM 139 159 4 (potential).
FT TOPO_DOM 160 184 Cytoplasmic (Potential).

FT TRANSMEM 185 205 5 (Potential).
FT TOPO_DOM 206 216 Extracellular (Potential).
FT TRANSMEM 217 237 6 (Potential).
FT TOPO_DOM 238 318 Cytoplasmic (Potential).
FT TRANSMEM 319 339 7 (Potential).
FT TOPO_DOM 340 366 Extracellular (Potential).
FT TRANSMEM 367 387 8 (Potential).
FT TOPO_DOM 388 398 Cytoplasmic (Potential).
FT TRANSMEM 399 419 9 (Potential).
FT TOPO_DOM 420 425 Extracellular (Potential).
FT TRANSMEM 426 446 10 (Potential).
FT TOPO_DOM 447 477 Cytoplasmic (Potential).
FT TRANSMEM 478 498 11 (Potential).
FT TOPO_DOM 499 504 Extracellular (Potential).
FT TRANSMEM 505 525 12 (Potential).
FT TOPO_DOM 526 530 Cytoplasmic (Potential).
FT CARBOHYD 356 356 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 129 187 Missing (in isoform AIM-1c).
FT VARSPLIC 188 295 Missing (in isoform AIM-1b).
FT VARSPLIC 386 406 YFQKVLVSTIGUKGLYFTGYL -> CKSFSLRLMSKSPWS
FT FTId=VSP_006298.
FT VARSPLIC 407 530 Missing (in isoform AIM-1b).
FT VARIANT 58 58 P -> A (in OCA4).
FT VARIANT 58 58 P -> S (in OCA4).
FT VARIANT 157 157 D -> N (in OCA4).
FT VARIANT 188 188 G -> V (in OCA4).
FT VARIANT 202 202 W -> C (in OCA4).
FT VARIANT 221 221 Missing (in OCA4).
FT VARIANT 272 272 E -> K.
FT VARIANT 317 317 Y -> C (in OCA4).
FT VARIANT 361 361 L -> P (in OCA4).
FT VARIANT 374 374 F -> L (common polymorphism;
FT dbSNP:168991982).
FT VARIANT 477 477 A -> T (in OCA4).
FT VARIANT 486 486 A -> V (in OCA4).
FT VARIANT 500 500 T -> P.
FT VARIANT 507 507 V -> L.
FT SEQUENCE 530 AA; 58302 MW; F14A4BACA8FF31B CRC64;
SQ
Query Match 17.1%; Score 488.5; DB 1; Length 530;
Best Local Similarity 26.4%; Pred. No. 9.8e-29;
Matches 150; Conservative 78; Mismatches 233; Indels 107; Gaps 12;
QY 8 SLLLRKAQLLLVNLTFGLBVCIAAGITYVPVLLLEVGVEEKFTMTWVGIGPVLGLVC 67
DB 33 SRLIWHSMAM-----FGREFCVAEAYVTPVLLSVGLPSSLSYIVWFLSPILGFL 84
QY 68 VFLGASADHWRGRRPFTIWSLGLLSLFIIPRAGWAGLICPPDR---PLELAL 124
DB 85 QPVGASDCHRSRGRRRPYILTGLVMVLGALYNGATVVAALIANPRKRLVWISV 144
QY 125 LILGVGLDFCCQVCFPLEALLSDFPRDPHCRQAYSVYAFMISLGGCIGYLLPAIDWD 184
DB 145 TMIGVWLFDAADFIDGPIKAYLFDVCSHODK-EKGLHYHALFTGFGGALGYLLGIDWA 203

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QY 185 TSALAPYLQTECLFGLTLTLFLCTVAATLLVAEEAALGPTPEAEGLSAPLSPHCCPC 244
Db 204 HLELGRLLGTGFQVFFSALVLTLCFTVHLCSISEAPL--TEVAKGI-PPQQTPODPPL 260
QY 245 RA-----RLAFNL-----GALLPRLHQLCCRPTRLRL 274
Db 261 SSDGMVEYSIEKVKNGYVNPPELAMQGANKNHAEQTRAMTLKSLLRALVNNPPHYRL 320
QY 275 FVAELCSNMALMTFTLFTDFVGEGLYQGVPRAPGTEARRHYDEGVRMGSLGLFLQCAI 334
Db 321 CTSHLIGWTAFLSNMLFFTFDFMGQIVYRGDPYSAHNSTEFLIYERGVGCGWGCINSVF 380
QY 335 SLVFSLMRLVORFTRAVYLASVAAPVPAAGATCLSHSVAVVTASAALTGFTFSALQI 394
Db 381 SLSYSFQKVLVSYIGLGLYFTGLYGLTGFTIGLFNNVSTLVCLSLFGVMSSTLYT 440
QY 395 LPYTLASLYHREKQVPLPKYRGDTGGASSEDLSMTSFLPGPKGAPFNGHVGAGSGLL 454
Db 441 VPFNLITEXHREEE---KEROQA-----PGDP----- 465
QY 455 PPPALCGASACDVSVRVVVGPTPEARVVGPRGICLDLAILDSAFLLSOVAPSLFMGSIV 514
Db 466 -----DNSVR-----GKG--MDCATLTCMVQLAQILVGGGLGLFLV 498
QY 515 QLSQSVTAYMVSAAAGLGLVAIYFATQV 542
Db 499 NTAGTVVVVITASAVALLGCCFVALFV 526

RESULT 15
Q7QG04 ANOGA
ID Q7QG04 ANOGA PRELIMINARY; PRT; 614 AA.
AC Q7QG04;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DE 07-FEB-2006, entry version 11.
DS ENSANGP0000018244 (Fragment).
GN ORFNames=ENSANGG0000015755;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxId=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAB01008823; BAA05502.2; -; Genomic_DNA.
DR InterPro; IPR000150; Hypoethet_cof.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; KFS_1; 1.
DR PROSITE; PS01228; COF_1; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 614
SQ SEQUENCE 614 AA; 67395 MW; FB02F9B8C88763ED CRC64;
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Query Match 17.1%; Score 488.5; DB 2; Length 614;
Best Local Similarity 22.7%; Pred. NO. 1.1e-28;
Matches 145; Conservative 104; Mismatches 220; Indels 171; Gaps 15;

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QY 8 SLLRHR-KAQLLVNLLTFFGLVCLAAQITVPPLLLEVGVVEKFTMTVLGIPVLGLV 66
Db 41 SHVFNKSRRDFIRISAVIMGMEFYSAETA VSPILLSIGIEHQMTVMWGISPLJGFF 100
QY 67 CVPILGASDHWGRYGRRRRPFIMWLSGILLSLFLPR-----AGWLA--GLLCPDPRL 120
Db 101 LSPVIGSVSDRCRSRFRGRRRPFVLFALGVGLITGCIILVYGRNIGAWFGDLGEVDDPANT 160
QY 121 -----ELALLILGVLLDFFCQVCF 140
Db 161 INGAALIDINGTVSDALRSYNFRIEBOIAEHRTDYRWAIVITIGILIDFNADCM 220
QY 141 TPLEALLSDFRDPDPCRQAVSYAFMISLGCGLGYLLPAIDWDTSALAPYLGTOECLF 200
Db 221 TFSRAFLDVLSPEDHGR-ACSTFSLAGLGSIGVAMGINWDETSFGEFLGSGIKTF 279
QY 201 GLLTILFTCVAATLLVAEEAALGPTPEAEGLSAPLSPHCCPCRAR-----LAFNLG- 254
Db 280 TLWVIFTICTLISLTSFREIPL-FLLESDDLRLPLTEAAIKKEKARRQNQIFVVKDVSK 338
QY 255 ALLPRLHQL-----CCR 266
Db 339 ALTAQLQSIQSDAVPQKINNALVDVERAPRGKDEVELVEEEDENVQMPDFIKSIYM 398
QY 267 MPRTLRLRFVABELCSNMALMTFTLFTDFVGEGLYQGVPRAPGTEARRHYDEGVRMGSL 326
Db 399 MPKSIATVCLTNLFCWMSHLVALYFTDFVGEVEFKGNPAAPSNDSDEYKLFLEGVRYACF 458
QY 327 GLFLQCAISLVFSLVMDRLVQRFGRVAVYLA SVAAPVPAAGATCL S-----HSVAVVTASAA 383
Db 459 GMAIYSISCSCTGFTIEKLIKVLRTVYCGGLIL--DAIGNMACMAFFPNKVTYVLSAT 516
QY 384 LTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSEDLSMTSFLPGPKGAPFN 443
Db 517 -GGIVYALLTFMPFLLLGQYHAK-----GTFKVAKPGA----- 548
QY 444 GHVGAGGSGLLPPPPALCGASACDVSVRVVVGPTPEARVVGPRGICLDLAILDSAPLLSQ 503
Db 549 -----EVTQER-----KRGLATDIAVVGGMIFVAQ 573
QY 504 VAPSLFMGSIVOLSOVSVTAYMVSAAAGLGLVAIYFATQVVF 543
Db 574 IIVALGMGSLISAFGTTSVVVFSASICSLSIASCASQVYV 613
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Search completed: May 27, 2006, 04:04:46
Job time : 307 secs

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